



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 114184

TO: Minh-Tam Davis
Location: rem/3a24/3c18
Art Unit: 1642
Tuesday, February 24, 2004

Case Serial Number: 10/032159

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Davis,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 09:51:41 ; Search time 7900 Seconds

(without alignments)
11268.272 Million cell updates/sec

Title: US-10-032-159a-19

Perfect score: 2176
Sequence: 1 accaccaggaagtcgacacag.....aaacagcaggggtgacccgc 2176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454613386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: 1: gb_da: 2: gb_hcg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pac: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pal: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_hcg_hum: 31: em_hcg_inv: 32: em_hcg_other: 33: em_hcg_mus: 34: em_hcg_pin: 35: em_hcg_rod: 36: em_hcg_mam: 37: em_hcg_vrt: 38: em_sy: 39: em_hcg_hum: 40: em_hcg_mus: 41: em_hcg_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	2176	100.0	2176	6	BD160313
2	2176	100.0	2176	9	AK024001
3	1757	80.7	2132	9	AF311287
4	1746	80.2	2098	6	AX154565
5	1448.4	65.4	1608	6	AX154567
6	1423.8	65.4	1836	6	BC008877
7	1060.2	48.7	1879	6	AX154562
8	1060.2	48.7	1879	10	AF311288
9	1045	48.0	1608	6	AX154564
10	725.4	33.3	765	6	BD150612
11	398	18.3	413	6	BD155532
12	389.8	17.9	188462	9	AL592301
13	374.8	17.2	2031	5	AB066061
14	373.8	17.2	4085	10	AY135367
15	372.2	17.1	3441	6	AX154573
16	372.2	17.1	3955	9	AF352576
17	372.2	17.1	4276	6	AX154571
18	372.2	17.1	4276	9	AF322641
19	372.2	17.1	4293	9	AK074049
20	365.8	16.8	2595	9	BC035805
21	323	14.8	179270	10	AC121918
22	323	14.8	213918	10	AL732541
23	264	12.1	3096	6	AX154570
24	264	12.1	3908	9	AY032928
25	264	12.1	3948	6	AX300499
26	264	12.1	3949	6	AX154568
27	264	12.1	3949	9	AY028896
28	261.6	12.0	241048	2	AC129824
29	261.2	12.0	4438	10	AF353456
30	175.4	8.1	711	6	AX300495
31	156.8	7.2	224198	2	AC106674
32	151.8	7.0	124088	10	AL929026
33	151.2	6.9	261474	2	AC094196
34	149	6.8	105327	5	AC140940
35	147.2	6.8	168210	2	AC116700
36	146.4	6.7	160539	2	AC109193
37	144.6	6.6	293592	2	AC094571
38	139.4	6.4	240931	2	AC107097
39	137.8	6.3	3682	9	AY032927
40	137.8	6.3	3931	9	AF322642
41	136.2	6.3	2621	9	BC018142
42	132.8	6.1	9551	6	AR076233
43	132.8	6.1	9551	6	I39845
44	132.8	6.1	9551	9	HMTHTRYAL
45	132.8	6.1	272545	2	AC090533

ALIGNMENTS

RESULT 1
LOCUS BD160313 2176 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD160313
VERSION BD160313.1 GI:27866071
KEYWORDS UP 2002191363-A/15156.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2176)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,T.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof

[illegible][illegible]

QY 781 AGCTAAGACACAGCTTCATGAAAGCCGAGAGCACTGCAAGGTGAGGCGAAGCAACAGC 840
 Db 781 AGCTAAGACACAGCTTCATGAAAGCCGAGAGCACTGCAAGGTGAGGCGAAGCAACAGC 840
 QY 841 TGAAGCTCAGGCAAGCCATGAGAGCAGGCGCCAGCAGAGCTGCTGTGGAGACTGCAAGC 900
 Db 841 TGAAGCTCAGGCAAGCCATGAGAGCAGGCGCCAGCAGAGCTGCTGTGTGGAGCTGCAAGC 900
 QY 901 AGAAGAGAGCCCTGCTCCAGAGCCCGGCTGCAAGAGCTGAGAGCCCTCCGTCAGAGAGGGA 960
 Db 901 AGAAGAGAGCCCTGCTCCAGAGCCCGGCTGCAAGAGCTGAGAGCCCTCCGTCAGAGAGGGA 960
 QY 961 AGGTGAGAGAGAGAGAGCCCTACATCAGAGTACTGAGAGAGAGAGTGGCGAGAGGCTGAGC 1020
 Db 961 AGGTGAGAGAGAGAGAGCCCTACATCAGAGTACTGAGAGAGAGAGTGGCGAGAGGCTGAGC 1020
 QY 1021 GGGAGCCAGAGAGAGAGAGCCCAACCATCTTCTCCCTGCGAAGAGACCTCCGCGAGAGGCG 1080
 Db 1021 GGGAGCCAGAGAGAGAGAGCCCAACCATCTTCTCCCTGCGAAGAGACCTCCGCGAGAGGCG 1080
 QY 1081 AGGCCCCAGAGCTCCGCTGCAAGAGAGAGAGAGAGTGTTCAGAGCTGCAAGTGTGCGAGC 1140
 Db 1081 AGGCCCCAGAGCTCCGCTGCAAGAGAGAGAGAGAGTGTTCAGAGCTGCAAGTGTGCGAGC 1140
 QY 1141 TAGGTAGAGATCTCCAGATGTACAAAGAGCCGATGAGAGCCATCTGCTGAGATGAGAGG 1200
 Db 1141 TAGGTAGAGATCTCCAGATGTACAAAGAGCCGATGAGAGCCATCTGCTGAGATGAGAGG 1200
 QY 1201 AGGTCCCATTTAGAGCGGAGCAAGAGAGCAAAATGAGAGGAGCTGTGACACAGCTCCGCGC 1260
 Db 1201 AGGTCCCATTTAGAGCGGAGCAAGAGAGCAAAATGAGAGGAGCTGTGACACAGCTCCGCGC 1260
 QY 1261 CCAGCGGCTTGAAGCTCCCGAGAGCTCTGCTTGAAGTGTGAGCGGCGCGAGCGCGCC 1320
 Db 1261 CCAGCGGCTTGAAGCTCCCGAGAGCTCTGCTTGAAGTGTGAGCGGCGCGAGCGCGCC 1320
 QY 1321 AGGCGAAGCTTGGGGCCCTTCACTGAGAGGTCGCTTGTGCTGTCCCTGACAGGCTATAGCC 1380
 Db 1321 AGGCGAAGCTTGGGGCCCTTCACTGAGAGGTCGCTTGTGCTGTCCCTGACAGGCTATAGCC 1380
 QY 1381 AGCCGGAGAGAGCTGAG 1440
 Db 1381 AGCCGGAGAGAGCTGAG 1440
 QY 1441 AAGCAGAGTGGAGAGCTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 Db 1441 AAGCAGAGTGGAGAGCTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 QY 1501 GAGGCGAGTACTGAGCGCTGAG 1560
 Db 1501 GAGGCGAGTACTGAGCGCTGAG 1560
 QY 1561 CTGAGCTCCAGCTCGAAGATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 Db 1561 CTGAGCTCCAGCTCGAAGATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 QY 1621 GACTGAG 1680
 Db 1621 GACTGAG 1680
 QY 1681 CAGGCTTTGAGAGTGCAG 1740
 Db 1681 CAGGCTTTGAGAGTGCAG 1740
 QY 1741 AGCAGCGGAG 1800
 Db 1741 AGCAGCGGAG 1800
 QY 1801 CGCAG 1860
 Db 1801 CGCAG 1860

QY 1861 GAGAAACACACAGGAG 1920
 Db 1861 GAGAAACACACAGGAG 1920
 QY 1921 CCGAG 1980
 Db 1921 CCGAG 1980
 QY 1981 ACTGCGGAG 2040
 Db 1981 ACTGCGGAG 2040
 QY 2041 CTCACACAG 2100
 Db 2041 CTCACACAG 2100
 QY 2101 TTAACACAG 2160
 Db 2101 TTAACACAG 2160
 QY 2161 AGCAGGAG 2176
 Db 2161 AGCAGGAG 2176

RESULT 3
 AF311287 2132 bp mRNA linear PRI 10-JAN-2001
 LOCUS Homo sapiens caspase recruitment domain protein 9 mRNA, complete
 DEFINITION
 cde.
 ACCESSION AF311287
 VERSION AF311287.1 GI:11066983
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 1 (bases 1 to 2132)
 Bertin,J., Guo,X., Wang,L., Srinivasula,S.M., Jacobson,M.D.,
 Poyet,J.-L., Merriam,S., Du,M.Q., Dyer,M.W.S., Robison,K.E.,
 Distefano,P.S., and Alnemri,E.S.
 CARD9 is a novel caspase recruitment domain-containing protein that
 interacts with Bcl10/CIAP and activates NF-kappa B
 J. Biol. Chem. 275 (52), 41082-41086 (2000)
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 11053425
 2 (bases 1 to 2132)
 Bertin,J.
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (05-OCT-2000) Neurobiology, Millennium Pharmaceuticals,
 Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
 FEATURES
 source
 1..2132
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 128..1738
 /function="binds to Bcl10/CIAP and activates NF-kB"
 /note="CARD9"
 /codon_start=1
 /product="caspase recruitment domain protein 9"
 /protein_id="AA028790.1"
 /translation="MSDYNDDECMNVLEGRVLTSTVIDPSRITPYLRCKVNPDD
 EOVLSDPNIVIRKRVGLDILORTGKGVAFLESLIYFOLYKVTGKBPARY
 FSVITDASGSGGLVOLLMTBVKIOKYODITALLSBDPIKLRPYDLSLRGHR
 VORLKEEASRELRCKENYDLAKLHOSKALMRNDLQJLEIOLKSLM
 KAEDCKVERHTLKLRAHMEORPSOELMLIOEKALORVOLEASVGBKIDRS
 SPYIVLEEDWRALRDHOANTIFSLRKDLRGEARLRCMEKEAFELICLALRK
 DSKWKRIETAILIOMEVVALEPOALITREELNAQHRGLQEDALRKQVREIGERA
 DELIQLVQCEAQLAVGRRLRQDLITLVLSLDEGSPRSQELSLPDLLEIOLK
 DKGLAGGSGSPKPPALHOSVLRNPDAGLSSGEPPEKRRRLKESFENYRRKRL
 RRMQKWRQGEEDRENTTGSNDITEGS"
 CDS
 128..1738
 /function="binds to Bcl10/CIAP and activates NF-kB"
 /note="CARD9"
 /codon_start=1
 /product="caspase recruitment domain protein 9"
 /protein_id="AA028790.1"
 /translation="MSDYNDDECMNVLEGRVLTSTVIDPSRITPYLRCKVNPDD
 EOVLSDPNIVIRKRVGLDILORTGKGVAFLESLIYFOLYKVTGKBPARY
 FSVITDASGSGGLVOLLMTBVKIOKYODITALLSBDPIKLRPYDLSLRGHR
 VORLKEEASRELRCKENYDLAKLHOSKALMRNDLQJLEIOLKSLM
 KAEDCKVERHTLKLRAHMEORPSOELMLIOEKALORVOLEASVGBKIDRS
 SPYIVLEEDWRALRDHOANTIFSLRKDLRGEARLRCMEKEAFELICLALRK
 DSKWKRIETAILIOMEVVALEPOALITREELNAQHRGLQEDALRKQVREIGERA
 DELIQLVQCEAQLAVGRRLRQDLITLVLSLDEGSPRSQELSLPDLLEIOLK
 DKGLAGGSGSPKPPALHOSVLRNPDAGLSSGEPPEKRRRLKESFENYRRKRL
 RRMQKWRQGEEDRENTTGSNDITEGS"

BASE COUNT 500 a 641 c 697 g 294 t
ORIGIN
Query Match 80.7%; Score 1757; DB 9; Length 2132;
Best Local Similarity 89.9%; Pred. No. 1,9e-249;
Matches 1999; Conservative 0; Mismatches 5; Indels 219; Gaps 2;
QY 25 CGCGGCTCTCTCCCTCCCTGCGAGCCCGGGGCGAGCTCTCCGAGAGGCTCCGGGGCCAG 84
DB 6 CGTCGGGCTCTCTCTCTCTCTGCGAGCCCGGGGCGAGCTCTCCGAGAGGCTCCGGGGCCAG 65
QY 85 GCTCTGCTGTGTCTGCTGAGTGCAGTGTCTCTGAGAGAGCCCTGAGCTCTGCTGAG 144
DB 66 GCTCTGCTGTGTCTGAGTGCAGTGTCTCTGAGAGAGCCCTGAGCTCTGCTGAG 125
QY 145 CCATGTCGAGCTACGAGAGAGATGAGATGTCTGAGAACGTCTGAGAGGCTTCCGGGTGA 204
DB 126 CCATGTCGAGCTACGAGAGAGATGAGATGTCTGAGAACGTCTGAGAGGCTTCCGGGTGA 185
QY 205 CGCTCACTCTGGTCACTGAGAGCCCTCAAGCATCAACCTTACCTGCGGCGAGTCAAGTCC 264
DB 186 CGCTCACTCTGGTCACTGAGAGCCCTCAAGCATCAACCTTACCTGCGGCGAGTCAAGTCC 245
QY 265 TGAACCTGATGATGAGAGAGAGAGTGTCTGAGAGCCCAACTGATCTATCCGAAACGGA 324
DB 246 TGAACCTGATGATGAGAGAGAGAGTGTCTGAGAGCCCAACTGATCTATCCGAAACGGA 305
QY 325 AAGTGGGTGTGTCTCTGAGCATCTGTGAGCGGACCGGCGCAAGAGGCTAGTGGCTTCC 384
DB 306 AAGTGGGTGTGTCTCTGAGCATCTGTGAGCGGACCGGCGCAAGAGGCTAGTGGCTTCC 365
QY 385 TCGAGAGCTTGAAGCTCTTACTACCCGAGCTGTACAAAGAGTCAAGAGGCTCAAGAGAGCCG 444
DB 366 TCGAGAGCTTGAAGCTCTTACTACCCGAGCTGTACAAAGAGTCAAGAGGCTCAAGAGAGCCG 425
QY 445 CCGGCGTCTCTCTCATGATATGAGAGCGGCTCCGGGAGTCAAGGCTCTGAGCTCTGA 504
DB 426 CCGGCGTCTCTCTCATGATATGAGAGCGGCTCCGGGAGTCAAGGCTCTGAGCTCTGA 485
QY 505 TGACTGAGTCACTGAGAGCTGAGAGAGAGTGCAGAGCTGACCGGCTGCTGAGCTCA 564
DB 486 TGACTGAGTCACTGAGAGCTGAGAGAGAGTGCAGAGCTGACCGGCTGCTGAGCTCA 545
QY 565 AAGATGACTTCACTCAAGAGAGCTGCGGTGAAGAGCAGCTCTGCGCAAGCAGAGAGC 624
DB 546 AAGATGACTTCACTCAAGAGAGCTGCGGTGAAGAGCAGCTCTGCGCAAGCAGAGAGC 605
QY 625 GTGTGCGAGAGCTTCAAGAGAGAGTGCAGAGCCCGGAGCCCGGAGCTTCAAGCGCTGCAAG 684
DB 606 GTGTGCGAGAGCTTCAAGAGAGAGTGCAGAGCCCGGAGCCCGGAGCTTCAAGCGCTGCAAG 665
QY 685 AGAGAGACTTCAAGAGAGCTGCGGCTGAGAGAGAGTGCAGAGAGTGCAGAGAGAGAGAGAGAG 744
DB 666 AGAGAGACTTCAAGAGAGCTGCGGCTGAGAGAGAGTGCAGAGAGAGAGAGAGAGAGAGAGAG 725
QY 745 TCAATGCGGAACCGTGAACCTGAGCTGAGATTGACCAAGCTCAAGCAGAGCTCATGAAG 804
DB 726 TCAATGCGGAACCGTGAACCTGAGCTGAGATTGACCAAGCTCAAGCAGAGCTCATGAAG 785
QY 805 CCGAGAGAGAGCTGAG 864
DB 786 CCGAGAGAGAGAGCTGAG 845
QY 865 AGCGGCGCGAG 924
DB 846 AGCGGCGCGAG 905
QY 925 GGGTGCAG 984
DB 906 GGGTGCAG 965
QY 985 TCCAGGTACTGAG 1044

DB 966 TCCAGGTACTGAG 1025
QY 1045 CCATCTTCTCCCTGCGAG 1104
DB 1026 CCATCTTCTCCCTGCGAG 1085
QY 1105 AGAGAGAGAGAGATGTTTCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1164
DB 1086 AGAGAGAGAGAGATGTTTCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1145
QY 1165 AG 1224
DB 1146 AG 1201
QY 1225 GCACAG 1284
DB 1202 ----- 1201
QY 1285 CCTGTGTTGAGTGTGGCGGCGGAG 1344
DB 1202 ----- 1201
QY 1345 AAGGTGCGGCTGT 1404
DB 1202 ----- CAGGCAATAGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1237
QY 1405 CAGGCGCGGAGCTTCAAG 1464
DB 1238 CAGGCGCGGAGCTTCAAG 1297
QY 1465 AAGGAG 1524
DB 1298 AAGGAG 1357
QY 1525 GGCAGAGCTCAGGCGGAG 1584
DB 1358 GGCAGAGCTCAGGCGGAG 1417
QY 1585 TCACCAG 1644
DB 1418 TCACCAG 1477
QY 1645 GACAAAGCTGTGCTTGTGCGGAG 1704
DB 1478 GACAAAGCTGTGCTTGTGCGGAG 1537
QY 1705 GAGCAGAGTGTGCGGAG 1764
DB 1538 GAGCAGAGTGTGCGGAG 1597
QY 1765 GAGCGGCGGAGCTTCAAG 1824
DB 1598 GAGCGGCGGAGCTTCAAG 1657
QY 1825 ATGAG 1884
DB 1658 ATGAG 1717
QY 1885 ACCGAGACTGAGAGAGCTTCAAG 1910
DB 1718 ACCGAGACTGAGAGAGCTTCAAG 1777
QY 1911 ----- -GAGAGCTTCCCGAG 1933
DB 1778 CCGGCGCTGCAACCGGAG 1837
QY 1934 GACTTGAGCTGAG 1993
DB 1838 GACTTGAGCTGAG 1897
QY 1994 GGGGCGGTTTGTAAAG 2053
DB 1898 GGGGCGGTTTGTAAAG 1957

QY	2054	TGCACAGGCATCTGTGTAATTTAGAGATCTGTTCTGTTTACCATTGTAACAGCAATATAC	2113
Db	1958	TGCACAGGCATCTGTGTAATTTAGAGATCTGTTCTGTTTACCATTGTAACAGCAATATAC	2017
QY	2114	ATGATGATGATGTATTAGTGTAGAAAAACAGAGCTGCTGTAATAATAACAGCAGGGTGAACC	2173
Db	2018	ATGATGATGATGTATTAGTGTAGAAAAACAGAGCTGCTGTAATAATAACAGCAGGGTGAACC	2077
QY	2174	CGC 2176	
Db	2078	CGC 2080	
RESULT 4			
AX154565			
LOCUS	AX154565	2098 bp	linear
DEFINITION	Sequence 4 from Patent WO0140468.		PAT 22-JUN-2001
ACCESSION	AX154565		
VERSION	AX154565.1	GI:14536158	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Bertin, J.		
AUTHORS	Molecules of the card-related protein family and uses thereof		
TITLE	Patent: WO 0140468-A 4 07-JUN-2001;		
JOURNAL	Millennium Pharmaceuticals, Inc. (US)		
FEATURES			
source	1..2098		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
	144..1754		
	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAC42605.1"		
	/db_xref="GI:14536159"		
	/translation="MSDYNDNDECMNVLEGFRTVLTSLVIDPSRTITPYLRCKVLANPDDP EEQVLSDNVLITRKRGVGLDILQRTGHKGVAFLEBLEYYQLYKRTGKPARV FSMTIDASGESGLTQLMTVEWKQKQYQODITALLSSKDDITKELRVDSLRRKQSE VORLKEBCEAGSRBELKREKNYDILAMLAHQSEKGLAMWRNDLQLEIDQLKSLMT KAEDDKVERKHTLKLRIAMFORPSOELMTLEOBEKALLQARVBLEVSQGLDSSK SPYLOVLEDMRKALRDHQEOANTIFSLKRDROGEARLRCEMEKEFELQCLALRRK DSKRTKRIEALILQMERVALERPOAATIREELIAOHARGIOEEDALRKQVRELGEKRX DELQQLVQCEAQLLAVEGRLRRQOLETVLTVSSLDLSDSPRSQELSIPQLEPTQLSS DKGLIAGGSSPKQPPALHQEVLNPNPDALSSGEPEKERRRRRLKESFENYRRKRAL RKMKQMGSGEEDENNTGSDNNTIGES"		
BASE COUNT	455 a	644 c	702 g 297 t
ORIGIN			
Query Match	80.2%	Score 1746;	DB 6; Length 2098;
Best Local Similarity	89.9%	Pred. No. 8e-248;	
Matches 1999;	Conservative	0; Mismatches	5; Indels 220; Gaps 3;
QY	25	CGGCGTCTCTCCCTCCCTCGTGAAGCCCGGAGAGATATCCACAGAGGCTCCGCGGCCAG	84
Db	22	CGTCGGGCTCTCCCTCCCTCGTGAAGCCCGGAGAGATATCCACAGAGGCTCCGCGGCCAG	81
QY	85	GCTCTGTGGTGTCTGCAGTGAAGGTGGCTCTGTGAAGAACCCTCAGCCTGCTGCTGAG	144
Db	82	GCTCTGTGGTGTCTGCAGTGAAGGTGGCTCTGTGAAGAACCCTCAGCCTGCTGCTGAG	141
QY	145	CCATGTCCGACTACGAGAACGATGACGAGTGTGGAACGTCCTGTGAAGGGCTTCCGGGTGA	204
Db	142	CCATGTCCGACTACGAGAACGATGACGAGTGTGGAACGTCCTGTGAAGGGCTTCCGGGTGA	201
QY	205	CGCTAAGCTCGGTATTCGACCCCTCAGCGATATACACTTACTCTGGGCAAGTGCAGATGCC	264
Db	202	CGCTAAGCTCGGTATTCGACCCCTCAGCGATATACACTTACTCTGGGCAAGTGCAGATGCC	261

Oy	265	TGAACCTGTAAGTAAAGAACAGAGTGTCTGACGACACCCCAACTGGTATATCCGACAAAGCA	324
Db	262	TGAACCTGTAGTAAAGAAAGAGGTGCTCAAGCGACCCCAACTGGTATATCCGACAAAGCA	321
Oy	325	AAGTGGGTGTGCTCTCTGACATCTCTGACAGGAGCACCGGCGCAAAAGGCTAGGTGGCTTCC	384
Db	322	AAGTGGGTGTGCTCTCTGACATCTCTGACAGGAGCACCGGCGCAAAAGGCTAGGTGGCTTCC	381
Oy	385	TCGAGAGCTTGAAGCTTAACTACCCGACGCTGTACAAAGAAAGTCAACAGGACAGAGCTCCG	444
Db	382	TCGAGAGCTTGAAGCTTAACTACCCGACGCTGTACAAAGAAAGTCAACAGGACAGAGCTCCG	441
Oy	445	CCCCGGCTTCTTCCATATGATCATGACGCCGTCCGGGGAGTCAAGGCTGAAGTGTGTGA	504
Db	442	CCCCGGCTTCTTCCATATGATCATGACGCCGTCCGGGGAGTCAAGGCTGAAGTGTGTGA	501
Oy	505	TGACTGAAGTCAATGAAGCTGACAAAGAGGTGACAGACTGACCGCGCTGTGAGTCTCA	564
Db	502	TGACTGAAGTCAATGAAGCTGACAAAGAGGTGACAGACTGACCGCGCTGTGAGTCTCA	561
Oy	565	AAATGACTTTCATCAAGAGAGTGGGGGTGAAGGACAGCTTGTGCGACACCAAGCA	624
Db	562	AAATGACTTTCATCAAGAGAGTGGGGGTGAAGGACAGCTTGTGCGACACCAAGCA	621
Oy	625	GTGTGCAAGGCTCAAGAGAGAGTGCAGAGGCTCCGACACCGGAGACTCAAGCGCTGCAAG	684
Db	622	GTGTGCAAGGCTCAAGAGAGAGTGCAGAGGCTCCGACACCGGAGACTCAAGCGCTGCAAG	681
Oy	685	AGAGAACTAAGACTGAGCTGAGGCTGAGCGGCGCACAGAGTGAAGAGAGAGGCGCGCGC	744
Db	682	AGAGAACTAAGACTGAGCTGAGGCTGAGCGGCGCACAGAGTGAAGAGAGAGGCGCGCGC	741
Oy	745	TCATGCGGAACCTGAGCTTGCAGCTGTGAGATTGACCAAGCTCAAGCACAGCTCATGAAG	804
Db	742	TCATGCGGAACCTGAGCTTGCAGCTGTGAGATTGACCAAGCTCAAGCACAGCTCATGAAG	801
Oy	805	CCGAGAGAGACTGCAAGGTGAGAGCGCAAGCACAGCTGAAGCTTAAGGCAAGCCATGAGC	864
Db	802	CCGAGAGAGACTGCAAGGTGAGAGCGCAAGCACAGCTGAAGCTTAAGGCAAGCCATGAGC	861
Oy	865	AGCGGGCCAGCAAGAGTGTGTGGAGCTGACAGCGAGAGAAAGCCCTGTCTCCAGGCCC	924
Db	862	AGCGGGCCAGCAAGAGTGTGTGGAGCTGACAGCGAGAGAAAGCCCTGTCTCCAGGCCC	921
Oy	925	GGGTGCAAGAGCTGAGGCTCTCCGTTCAGAGAGGAGAAAGCTGACAGAGAGAGCCCTTACA	984
Db	922	GGGTGCAAGAGCTGAGGCTCTCCGTTCAGAGAGGAGAAAGCTGACAGAGAGAGCCCTTACA	981
Oy	985	TCCAGAGTACTGAGAGAGAGACTTGCGCGGCGAGGCTGTCCGGAGCCACACAGAGAGCCACA	1044
Db	982	TCCAGAGTACTGAGAGAGAGACTTGCGCGGCGAGGCTGTCCGGAGCCACACAGAGAGCCACA	1041
Oy	1045	CCATCTTCTCCCTGCGCAAGGACCTCCGCGCAAGGGCGAGGCCCGACGCTCCGGTGCATGG	1104
Db	1042	CCATCTTCTCCCTGCGCAAGGACCTCCGCGCAAGGGCGAGGCCCGACGCTCCGGTGCATGG	1101
Oy	1105	AGAGAAAGAGATGTTTCAGCTGACAGTGCCTGCGCACTACGTAAAGACTCCAAGATGTACA	1164
Db	1102	AGAGAAAGAGATGTTTCAGCTGACAGTGCCTGCGCACTACGTAAAGACTCCAAGATGTACA	1161
Oy	1165	AGAGCCGATGAGAGCCATCTCTGCTGACAGATGAGAGAGGTGGCCATTAGCGGAGCCACA	1222
Db	1162	AGAGCCGATGAGAGCCATCTCTGCTGACAGATGAGAGAGGTGGCCATTAGCGGAGCCACA	1221
Oy	1225	GCACACAAATGAGAGGGGTGTGACCAAGCTCCGGGCCAAGGGGCTTGACGTCTCCGGAG	1288
Db	1218	-----	1217
Oy	1285	CCTCTGTTGAGATTGGCGCGCGCGGCCAGAGGGCCACAGGCAAGCTTGGGGCTTCACTG	1344
Db	1218	-----	1217
Oy	1345	AGGATCGGACCTTGTGCTGTCCCGCTAGGCGCATAGCCACGCGGAGAGAGCTGCACGACACAG	1404


```

Db      1218 -----CAGGCCATAGCCACCGGGAGAGGCTGCACGACAG 1253
QY      1405 CACGCCCGGGGCTGCAAGAGAGACCGGCTGCGCAAGCAGGTGGGAGCTGGGCGAG 1464
Db      1254 CACGCCCGGGGCTGCAAGAGAGACCGGCTGCGCAAGCAGGTGGGAGCTGGGCGAG 1313
QY      1465 AAGCGGATAGCTGACAGCTGACAGGTTCAGGTGAGAGCGGACGCTACTGGCCGGAG 1524
Db      1314 AAGCGGATAGCTGACAGCTGACAGGTTCAGGTGAGAGCGGACGCTACTGGCCGGAG 1373
QY      1525 GCGAGCTCAGCGGCGAGCAGCTGAGAGCGCTGCTGAGCTCCGACCTGGAAGATGAC 1584
Db      1374 GCGAGCTCAGCGGCGAGCAGCTGAGAGCGCTGCTGAGCTCCGACCTGGAAGATGAC 1433
QY      1585 TCACCCAGAGGTCCTCAGAGGCTTCACTCCCGAGAGCCTGAGAGCAACCCAGCTCTCA 1644
Db      1434 TCACCCAGAGGTCCTCAGAGGCTTCACTCCCGAGAGCCTGAGAGCAACCCAGCTCTCA 1493
QY      1645 GACAAAGGCTGCTTGCCTGGCGGGGAGGCCGAAACAGCCCTTTGCACTCTGCACAG 1704
Db      1494 GACAAAGGCTGCTTGCCTGGCGGGGAGGCCGAAACAGCCCTTTGCACTCTGCACAG 1553
QY      1705 GACGAGGTTTGGGGAACCCCATGACGAGGCTGAGAGCGGGAGCGCCCGAGAG 1764
Db      1554 GACGAGGTTTGGGGAACCCCATGAGCAGGCTTGAAGCGGGAGCGCCCGAGAG 1613
QY      1765 GAGCGGCGGCGCTCAAGAGAGTTTGAAGTCAACGAGAGAGCGGCTCAGAGAG 1824
Db      1614 GAGCGGCGGCGCTCAAGAGAGTTTGAAGTCAACGAGAGAGCGGCTCAGAGAG 1673
QY      1825 ATGAGAGAGATGCGCGGAGGGGAGAGAGACCGGAGAACCAACGCGGACGCAAC 1884
Db      1674 ATGAGAGAGATGCGCGGAGGGGAGAGAGACCGGAGAACCAACGCGGACGCAAC 1733
QY      1885 ACCGACACTAGGCTCTTAGCCGCA----- 1910
Db      1734 ACCGACACTAGGCTCTTAGCCGCAAGCGAGCGGACCGGACGAGGACCAACCGG 1793
QY      1911 -----GCAGACTTCCCGGAGCGCTGCT 1933
Db      1794 CCGCGCTGCGCACCGCGGGGTGCCAGCGCCTCGGGGCGCAGACTTCCCGAGCGCTGCT 1853
QY      1934 GACTTGGCTGGAACGAGATCTGTGCTGCTGAAAGGCCAGCGGACTGCGGCGATT 1993
Db      1854 GACTTGGCTGGAACGAGATCTGTGCTGCTGAAAGGCCAGCGGACTGCGGCGATT 1913
QY      1994 GGGGCGCTTTGTTAAGCGGCACTGATTTGCGAGGCGCATGCGGCTGCTCAACCCCA 2053
Db      1914 GGGGCGCTTTGTTAAGCGGCACTGATTTGCGAGGCGCATGCGGCTGCTCAACCCCA 1973
QY      2054 TGCAACGCGCATCTGTAACTTAAGATCTGTGCTTTCACCATGTAACAACAATAC 2113
Db      1974 TGCAACGCGCATCTGTAACTTAAGATCTGTGCTTTCACCATGTAACAACAATAC 2033
QY      2114 ATGATGATCTTGTATTTGTGTTT-AGAAACACAGCTGCGTAATAAACAACAAGGAG 2172
Db      2034 ATGATGATCTTGTATTTGTGTTT-AGAAACACAGCTGCGTAATAAACAACAAGGAG 2093
QY      2173 CCGC 2176
Db      2094 CCGC 2097

```

```

RESULT 5
LOCUS      AX154567      1608 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 6 from Patent WO0140468.
ACCESSION  AX154567
VERSION     AX154567.1 GI:14536160
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

```

```

REFERENCE
1 Bertin, J.
AUTHORS
TITLE      Molecules of the card-related protein family and uses thereof
JOURNAL    Patent: WO 0140468-A 6 07-JUN-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source     1..1608
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT 362 a 475 c 561 g 210 t
ORIGIN
Query Match 66.6%; Score 1448.4; DB 6; Length 1608;
Best Local Similarity 91.5%; Pred. No. 5.9e-204;
Matches 1607; Conservative 0; Mismatches 1; Indels 148; Gaps 1;
QY      147 ATGTGGACTGAGAGAGATGACGAGTGTGGAACGTCCTGAGAGGCTTCCGGGTGACG 206
Db      1 ATGTGGACTGAGAGAGATGACGAGTGTGGAACGTCCTGAGAGGCTTCCGGGTGACG 60
QY      207 CTACACTGGTATCAGACCCCTCAAGCATCAACCTTACTCTGCGCAGTGAAGTCTCTG 266
Db      61 CTACACTGGTATCAGACCCCTCAAGCATCAACCTTACTCTGCGCAGTGAAGTCTCTG 120
QY      267 AACCTGTATGAGAGACAGGTGCTAGGACCCCAACCTGTATCTCGAAGCGAAA 326
Db      121 AACCTGTATGAGAGACAGGTGCTAGGACCCCAACCTGTATCTCGAAGCGAAA 180
QY      327 GTGGTGTGCTCTTGAATCTCTGACGAGCGGCGCAAGGGCTTAGTGCTTCTCT 386
Db      181 GTGGTGTGCTCTTGAATCTCTGACGAGCGGCGCAAGGGCTTAGTGCTTCTCT 240
QY      387 GAGAGCTGAGGCTTACTACCCGAGCTTAAAGAGTCAAGGAGGAGCCGCGC 446
Db      241 GAGAGCTGAGGCTTACTACCCGAGCTTAAAGAGTCAAGGAGGAGCCGCGC 300
QY      447 CGGCTCTTCCATCATCATCAACGCTCCGGGAGTCAAGGCTGACTCAGCTGCTGATG 506
Db      301 CGGCTCTTCCATCATCATCAACGCTCCGGGAGTCAAGGCTGACTCAGCTGCTGATG 360
QY      507 ACTGAGTCAATGAAGCTGCAAGAGGTGCAAGACTGACCGGCTGCTGAGCTTCAAA 566
Db      361 ACTGAGTCAATGAAGCTGCAAGAGGTGCAAGACTGACCGGCTGCTGAGCTTCAAA 420
QY      567 GATGACTTCAATGAAGAGTGTGGGTGAAGACAGCTGCTGCGCAAGCACTGAAGAGCT 626
Db      421 GATGACTTCAATGAAGAGTGTGGGTGAAGACAGCTGCTGCGCAAGCACTGAAGAGCT 480
QY      627 TGCGAGAGCTCAAGAGAGTGTGAGGCGCGGCAAGCTCAAGGCTGCAAGAGG 686
Db      481 TGCGAGAGCTCAAGAGAGTGTGAGGCGCGGCAAGCTCAAGGCTGCAAGAGG 540
QY      687 GAGAACTAAGACTGCGGCTGCGGCTGCGGCAAGAGTGAAGAGAGAGAGGCGCGGCTC 746
Db      541 GAGAACTAAGACTGCGGCTGCGGCTGCGGCAAGAGTGAAGAGAGAGAGGCGCGGCTC 600
QY      747 ATGCGGACCGTGAAGCTGAGATTAACAGCTCAAGCAAGCTCATGAAGGCTC 806
Db      601 ATGCGGACCGTGAAGCTGAGATTAACAGCTCAAGCAAGCTCATGAAGGCTC 660
QY      807 GAGAGACACTGAGAGTGAAGCGCAAGCAAGCTGAGAGCTCAAGGACGCTATGAGAGC 866
Db      661 GAGAGACACTGAGAGTGAAGCGCAAGCAAGCTGAGAGCTCAAGGACGCTATGAGAGC 720
QY      867 CGGCCAGCGCAGAGTGTGTGAGAGCTGCGAGAGAGAGAGAGGCTGCTCAAGGCGCGG 926
Db      721 CGGCCAGCGCAGAGTGTGTGAGAGCTGCGAGAGAGAGAGAGGCTGCTCAAGGCGCGG 780
QY      927 GTGCAAGCTGAGAGCTCCGTCAGAGAGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 986

```


Gene

CDS

1. 1836
/gene="CARD9"
/db_xref="LocusID:64170"
/db_xref="MIM:607212"
151. 1629
/codon_start=1
/product="caspase recruitment domain protein 9, isoform 2"
/protein_id="AAH08877.1"
/db_xref="GI:14250814"
/db_xref="LocusID:64170"
/translation="MSDYNDDECSVLEGFRTVLTSPVSRITPYLRCKLVNDP
EEOVLSDPNIVLRKRVGLDILORTGKGVYAFLESLEIYYPOLYKVKREPARV
FSTITDASGSSGLTQILMTWVKLQKKVDLTALLSKDPFIKEALVKDSLKHDER
VQRLKECEAGSRELKCKEENDLMLRHLAHOSEKALMRDLQLEIDQLKSLM
KAEDKVERKHTKLRLHAMEORPSOELMELQOEKALQARVQELASVQGLDRS
SPYIVLEEDMRQALRDHOEANTIFSLRKLQGEARLRCEKEKEMELQCLMRK
DSKMYDRITAILQMEVAILRDQALIRREELHAHQALRQVAREVLEKKA
DELOLVQCEADLLAVEGRILRQLEFVLTSSLDLSDGSPRSQELSLFDLLEDTQLS
DKGLAGGSFKQPFALHROEVLNPNHAGPGLPGAVC"

BASE COUNT
ORIGIN

Query Match 65.4%; Score 1423.8; DB 9; Length 1836;
Best Local Similarity 91.3%; Pred. No. 2,4e-200;
Matches 1583; Conservative 0; Mismatches 2; Indels 148; Gaps 1;

QY 6 CAGGAATGACAGAGCGCTCCGCGGTGCTCTCCCTCCCTGACAGCCCGGAGACATCTCC 65
Db 10 CAGGAATGACAGAGCGCTCCGCGGTGCTCTCCCTCCCTGACAGCCCGGAGACATCTCC 69
QY 66 CAGAGCTCCGCGCCCGAGGCTCTCGTGTGTCTGACAGTACAGAGGCTCTTGAAGACC 125
Db 70 CAGAGCTCCGCGCCCGAGGCTCTCGTGTGTCTGACAGTACAGAGGCTCTTGAAGACC 129
QY 126 CTGAGCTGCTGCTGAGGCGATGTGCGACTACAGAACGATGACGATGCTGAACGTC 185
Db 130 CTGAGCTGCTGCTGAGGCGATGTGCGACTACAGAACGATGACGATGCTGAACGTC 189
QY 186 CTGAGAGGCTTCCGGGTGAGCTCACTCGGTATGAGACCTCCAGCATCAACTTAC 245
Db 190 CTGAGAGGCTTCCGGGTGAGCTCACTCGGTATGAGACCTCCAGCATCAACTTAC 249
QY 246 CTGCGGAGTGAAGGCTGAAACCTGATGAGAGGAGGAGTGTCCAGCGACCCCAAC 305
Db 250 CTGCGGAGTGAAGGCTGAAACCTGATGAGAGGAGGAGTGTCCAGCGACCCCAAC 309
QY 306 CTGCTCATCCGAAACGGAAGTGGGTGTCTCTTGAACATCTCTGACGAGCCGAC 365
Db 310 CTGCTCATCCGAAACGGAAGTGGGTGTCTCTTGAACATCTCTGACGAGCCGAC 369
QY 366 AAGGCTACGTGCTTCTCTGAGAGCTTGAAGCTTACTACCGGAGCTGTACAAAG 425
Db 370 AAGGCTACGTGCTTCTCTGAGAGCTTGAAGCTTACTACCGGAGCTGTACAAAG 429
QY 426 GTACAGGCAAGAGCCGCGCGCTTCTCAATGATCATGACCGCTCCGGAGTCA 485
Db 430 GTACAGGCAAGAGCCGCGCGCTTCTCAATGATCATGACCGCTCCGGAGTCA 489
QY 486 GGGCTGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
Db 490 GGGCTGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
QY 546 ACCGCGCTGCTGATCTCAAGATGATCACTTCAAGAGCTGCGGATGAGAGCAAGCTG 605
Db 550 ACCGCGCTGCTGATCTCAAGATGATCACTTCAAGAGCTGCGGATGAGAGCAAGCTG 609
QY 606 CTGCGCAAGCAAGAGCGTGTGTCAGAGGCTCAAGAGGAGTGTGCAAGCGCGGACCGC 665
Db 610 CTGCGCAAGCAAGAGCGTGTGTCAGAGGCTCAAGAGGAGTGTGCAAGCGCGGACCGC 669
QY 666 GAGTCAAGGCTGTCAGAGGAGAGAACTAGACTTGCCCTGCGCTGCGGACCAAGAT 725
Db 670 GAGTCAAGGCTGTCAGAGGAGAGAACTAGACTTGCCCTGCGCTGCGGACCAAGAT 729

QY 726 GAGGAGAGGCGCGCGCTCATGCGGAAACCGTGAACCTTGCAGCTTGAGATTGACAGCTC 785
Db 730 GAGGAGAGGCGCGCGCTCATGCGGAAACCGTGAACCTTGCAGCTTGAGATTGACAGCTC 789
QY 786 AAGCAAGCTCATGAGAGCGGAGAGAGAGTGAAGGTGAGCGGACCAAGCTGTAAG 845
Db 790 AAGCAAGCTCATGAGAGCGGAGAGAGAGTGAAGGTGAGCGGACCAAGCTGTAAG 849
QY 846 CTGAGCAAGCCATGAGAGAGAGCGGAGAGAGTGAAGGTGAGCGGAGCTGAGAGAGAG 905
Db 850 CTGAGCAAGCCATGAGAGAGAGCGGAGAGAGTGAAGGTGAGCGGAGCTGAGAGAGAG 909
QY 906 AAGGCTGCTTCCAGGCGCGGATGAGAGGCTTCCGCTCAAGAGAGAGAGCTG 965
Db 910 AAGGCTGCTTCCAGGCGCGGATGAGAGGCTTCCGCTCAAGAGAGAGAGCTG 969
QY 966 GACAG 1025
Db 970 GACAG 1029
QY 1026 CACGAG 1085
Db 1030 CACGAG 1089
QY 1086 CGAGCGCTCCGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1145
Db 1090 CGAGCGCTCCGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149
QY 1146 AAGAGCTCAAGATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1205
Db 1150 AAGAGCTCAAGATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1209
QY 1206 GGCATTGAGCGGAG 1265
Db 1210 GGCATTGAGCGGAG 1269
QY 1266 GGCATTGAGCGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
Db 1225 ----- 1224
QY 1326 AAGCTTGGGCGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1385
Db 1225 ----- 1224
QY 1386 GAGAGAGTGCAGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1445
Db 1242 GAGAGAGTGCAGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1301
QY 1446 GGTGCGGAGAGTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1505
Db 1302 GGTGCGGAGAGTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1361
QY 1506 GAGCTACGCGCGGAG 1565
Db 1362 GAGCTACGCGCGGAG 1421
QY 1566 CTCCAGCTGGAAGATGCTCAACAGAGAGTCCAGAGAGCTTCACTCCCCAGAGAGCT 1625
Db 1422 CTCCAGCTGGAAGATGCTCAACAGAGAGTCCAGAGAGCTTCACTCCCCAGAGAGCT 1481
QY 1626 GAGAGACACCAAGCTTCAAGCAAAAGGCTGCTTCCGCGCGGAGAGAGAGAGAGAG 1685
Db 1482 GAGAGACACCAAGCTTCAAGCAAAAGGCTGCTTCCGCGCGGAGAGAGAGAGAGAG 1541
QY 1686 CTTTGAGAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1738
Db 1542 CTTTGAGAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1594

RESULT 7
AX154562
LOCUS AX154562 1879 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1 from Patent WO0140468.
ACCESSION AX154562
VERSION AX154562.1 GI:14536155
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Bertin J.
TITLE Molecules of the card-related protein family and uses thereof
JOURNAL Patent: WO 0140468-A 1 07-JUN-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1.1879
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
113..1173
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC42604.1"
/db_xref="GI:14536156"
/translation="MSDYENDECSWALSFRVRLISVIDPSRIPTYLRQCKVLPND
EBOVLSDPVLVIRKRVGLDILORTGHGVAFLESELYPOLYRKVTKGEFARV
FSEITDASESGITOLIMTEWKLQKQODLTALLSKDDPIKELRATVDSILRKQER
VQRLKECELSSELKRCRDENYDLMRLHLSEKALMNRDLQLEVDQRLISM
KAEDDCKVRKHTLKLRLHMBQRPSQELMLQSERDILQAVQLEVEVQELKLRN
SPYIQLYEDRWQALQEHQEOASTIFSLKDLROALATRCMEKEVEFELQALRK
DAWYDRLEALIQWEEVSIERDQMTGRELHAQCSFQDKXLRQVYELDEKA
DELQIQLPOTSERLAABGRLLQOQLODMTILSSDLENSPREPSQLSLPDLLENAL
SLKGVTLADESPQRPVYLNKXHLSTHTVSSSEPPKERRRLKESYENRRRLAL
RKQNSWRQGEHGHNTGSDMTDTGS"
BASE COUNT 496 a 503 c 578 g 302 t
ORIGIN
Query Match 48.7%; Score 1060.2; DB 6; Length 1879;
Best Local Similarity 76.2%; Pred. No. 9e-147;
Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4;
QY 76 GCGGCCAGGCTCTGCTGTGTGTCAGAGTCAGAGTGTCTCTGGAAGACCTCAGGCTGC 135
DB 46 GTGCCATATGCCAGGACATCAGCTGACAGGTGCTCCACAGACCTTGA-----GC 101
QY 136 CTGCTAGGCGCATGTGCGACTACAGAGAGATGACAGTGTGGAACGTCTTGAGGGCT 195
DB 102 CTACAGAGGACATGTAGACTATGAAATGACAGAGTGTGAGTGCCTTGAGAGCT 161
QY 196 TCCGGGTGACGCTACCTCGGTGATCAGACCTCAGCATCACAACCTTACCTGCGGAGT 255
DB 162 TCCGGGTGAGGTAATCTCTGTATGACCCCTCAGGAATCACACCTTATGCGGCACT 221
QY 256 GCAAGTCTCGAACCTCGATGATGAGAGAGAGTGTCTACGACGCCCAACCTGTATCATC 315
DB 222 GCAAGTCTCGAACCCCGATGATGAGAGAGAGTGTCTAGTAGCCCAACCTGTGTATCC 281
QY 316 GCAACGGAAGTGGTGTCTCTCTGGAACATCTCTGACGCGACCGGCCACAGAGGCTAGC 375
DB 282 GCAAGCGGAAGTGGTGTCTCTCTGGAACATCTCTGACGCGACCGGCCACAGAGGCTAGC 341
QY 376 TGGCTTCTCGAGAGGCTGAGCTCTACTACCCGAGCTGTACAAAGGTTCAGAGGCA 435
DB 342 TGGCTTCTTGAAGCTGGAACCTACTACCTCAGTTATACAGAAAGTCACTGGA 401
QY 436 AGAGACCGGCGCGGCTTTCTTCATGATCATGACGCGTCCGGGAGTCAAGGCTTACTG 495
DB 402 AGGAGCGGAGCGCGTGTCTTCTTCATGATCATGACGCGTCCGGGAGTCAAGGCTTACTG 461
QY 496 AGTGTGATGATGAGGCTGATGAGGCTGAGAAAGAGTGCAGAGCTGAGACCGGCTGC 555
DB 462 AGTGTGATGATGAGGCTGATGAGGCTGAGAAAGAGTTCAGAGCTGAGACCGGCTTTC 521

QY 556 TGAAGTCCAAAGATGATTTCTATGAGAGAGTGGCGGAGGAGAGACAGCTGTGGGAGC 615
DB 522 TGAAGTCCAAAGATGATTTCTATGAGAGAGTGGCGGAGGAGAGACAGCTTCTGGGAGC 581
QY 616 ACCAGAGCGGTGTCAGAGGCTCAAGAGAGAGTGCAGAGCGGAGCGGAGCTCAAGC 675
DB 582 ACCAGAGCGGAGTGCAGAGGCTCAAGAGAGAGTGTAGCTGAGACAGTGCAGAGCTGAGC 641
QY 676 GCTCAAGAGAGAGATCAAGACCTGACCTGCGCTGCGGACACAGAGTGAAGAGAG 735
DB 642 GCTCAAGAGATGAGAACTAGACCTGACCTGCGCTGCGGACACAGAGTGAAGAGAG 701
QY 736 GCGCGCGGCTCATCGGAAACCGTGAACCTGACGCTGAGAGATTGACCACTCAAGACAGC 795
DB 702 GAGCAGACCTCATCGGAAACCGTGAACCTGACGCTTGAAGTGAACCACTCAAGCAGCAGC 761
QY 796 TCATGAAGGCGGAGAGAGAGCTGCAAGGTGAGAGGAGAGAGAGAGAGAGAGAGAGAG 855
DB 762 TCATGAAGGCGGAGAGAGAGCTGCAAGGTGAGAGGAGAGAGAGAGAGAGAGAGAGAG 821
QY 856 CCATGAG 915
DB 822 CCATGAG 881
QY 916 TCAAGGCGCGGAGTCAAG 975
DB 882 TCAAGGCGCGGAGTCAAG 941
QY 976 GCGGCTTATCTCAAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1035
DB 942 GCGGCTTATCTCAAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
QY 1036 AGGCAACACCATTTCTCCCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1095
DB 1002 AGGCAACACCATTTCTCCCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1061
QY 1096 GGTGATGAG 1155
DB 1062 GGTGATGAG 1121
QY 1156 AGATGTCAG 1215
DB 1122 AGATGTCAG 1181
QY 1216 GAGAGCAG 1275
DB 1182 GAGAGC----- 1186
QY 1276 CCTCCGAGAGCTTGTGTTGAGAGTGGGCGCGCGGAGAGAGAGAGAGAGAGAGAGAG 1335
DB 1187 ----- 1186
QY 1336 CCTCTACTGAGAGTGTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1395
DB 1187 -----CAGGTATGAGCTCAAGGAGAGAGCTG 1213
QY 1396 CACGACAGACAGCGCGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1455
DB 1214 CATGACAGTGTGCGCAAGAGCTTTCAGGACAAAGATTAAGTGTGCGCAAGAGAGAGAG 1273
QY 1456 CTGGGCGGAG 1515
DB 1274 CTGGATGAG 1333
QY 1516 GCGGAG 1575
DB 1334 GCGGAG 1393
QY 1576 GAAAGTGGCTCAACAG 1632
DB 1394 GAAAGCAAGTCCCGAT 1453
QY 1632 ACCAGCTCTCAAGACAAAGAGCTGCTTGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1692

Db 1454 GCCAGCTCTCAACAAGGTCTCTGGAGACAGGAGAGGCCCAAGACAGCCTCTCGTG 1513
QY 1693 GCTTCGACACGAGAGGTTTTCGGAACCCCATGACGAGCCTGACAGCGGGAG 1752
Db 1514 GTTCTGAACAAGAGCATCTTTCGAGAG---CCATGACACGCTGCTCCAGCAGCAGAG 1570
QY 1753 CCGCCGAGAGAGAGCGCGCGCTCTCAAGAGAGTTTGAAGACTTACCGCAGGAAGCCG 1812
Db 1571 CCCCCGAGAGAGAGCGCGCGCTCTCAAGAGAGCTTCAAGAGACTTACCGCAGGAAGCCG 1630
QY 1813 GCCCTGAGAGAGTGCAGAAAGATGCGCGCAGAGGAGAGAGAGCAGGAGAACACACAG 1872
Db 1631 GCGCTCCGACAGATGCAAGACAGTGCACAGAGAGAGAGAGAGATACAGGAAATACAGCA 1690
QY 1873 GGCAGCAGACACACGACACTGAGAGGCTCTTACGCGCAGACAGACTTCCCGAGCGCTGC 1932
Db 1691 GGCAGCAGACACACGACACTGAGAGGCTCTTACAGAGACACAGCGCAGAGGCTGCTGT 1750
QY 1933 TGACTTGGCTGGAACG 1949
Db 1751 GTAATTGTGAAGGATG 1767

RESULT 8
AF311288 1879 bp mRNA linear ROD 10-JAN-2001
LOCUS Rattus norvegicus caspase recruitment domain protein 9 mRNA,
DEFINITION complete cds.
ACCESSION AF311288
VERSION AF311288.1 GI:11066985
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1879)
Bertin,J., Guo,Y., Wang,L., Srinivasula,S.M., Jacobson,M.D.,
Poyet,J.-L., Merriem,S., Du,M.Q., Dyer,M.J.S., Robison,K.E.,
D'Stefano,P.S. and Alnemri,E.S.
CARD9 is a novel caspase recruitment domain-containing protein that
interacts with Bcl10/CLAP and activates NF-kappa B
J Biol. Chem. 275 (52), 41082-41086 (2000)
JOURNAL MEDLINE 20576268
PUBMED 11053425
REFERENCE 2 (bases 1 to 1879)
Bertin,J.
Direct Submission
Submitted (05-OCT-2000) Neurobiology, Millennium Pharmaceuticals,
Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
JOURNAL TITLE Location/Qualifiers
FEATURES
source
1..1879
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
113..1723
/function="binds to Bcl10/CLAP and activates NF-kB"
/note="CARD9"
/codon_start=1
/product="caspase recruitment domain protein 9"
/protein_id="AA028791.1"
/db_xref="GI:11066986"
/translation="MSDYNDDECMALSFRLKLSIVDPRIITPYLRCKYLNPD
EBOVLSPNLVIRKVGVLIDLPFGHGVAFLSLSLYPOLYRKVTGEPARV
FSMTIDASGSGELTQIMTYMKQKRVQTLALSKDPFKELPKVSLAKHQR
VQRLKECELSAELEKRCXDEVIDLARLHLSEKGAALRNNDLQLEVDLRSLM
KAEDDCVERKHTKJLHAMEQRPQSELMDLQERDLQAEALRCEKEMFLQCLARK
SPYQVLEEDWRQALQEHQCASTIFSLRDLQAEALRCEKEMFLQCLARK
DAKVKDRIEALIQEWEVSIERDOANTSREELIAQCAQSGKDKLRKQVRELEDA
DELOLOPQRESRLAAGRLKKOOLMLTSSDLSESPRNSGELSLPDLBEDAOL
SDKGVADRESPEQPIVVLNKKHLSQTHDVTSSSEPEKERRLKESFENYRKAL

BASE COUNT 496 a 503 c 578 g 302 t
ORIGIN
RMONSWROEGDHGNTTGSNDTDEGS"
Query Match 48.7%; Score 1060.2; DB 10; Length 1879;
Best Local Similarity 76.2%; Pred. No. 9e-147;
Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4;
QY 76 GCGGCCACAGGCTCTGCTGTGTGTCTGCAAGTGAAGTGGTCTCTGGAAGACCTTCAAGCTGC 135
Db 46 GTGCCATATAGCCACAGCGACATCCAGCTGAGAGTGGTCTCCACAGACCTTGA---GC 101
QY 126 CTGCTAGAGCCATGCGGACTACGAGAACATGACGAGTGTGAGACGTCTGAGAGGCT 195
Db 102 CTACAGAGACATGTCATATGAAATGACGAGAGTGTGAGTGTCTTGAAGTCT 161
QY 196 TCCGGGTAGCCTCACTTGTGATCGACCCCTCAGCATACACTTACCTGCGGAGT 255
Db 162 TCCGGGTAGAGTAATCTTGTGATTCACCCCTCAGCATACACTTATCTGCGGAGT 221
QY 256 GCAGAGTCTGAAACCTGATGATGAGAGAGAGTGTGAGAGCCGACCCCACTGTGATCC 315
Db 222 GCAAGTCTTGAAACCCGATGATGAGAGAGAGTGTGAGAGCCGACCCCACTGTGATCC 281
QY 316 GCAAGCGAAAGTGGTGTCTCTTGTGATCTCTGACAGCGACCGGCAAGGGCTACG 375
Db 282 GCAGAGAGAGTGGTGTGTCTCTTGTGATCTCTGACAGCGACCGGCAAGGGCTACG 341
QY 376 TGGCTTCTCTGAGAGCCCTGAGAGCTCTACCTACCGCAGCTGTACAGAGGTCAAGGCA 435
Db 342 TGGCTTCTCTGAGAGCTCTGAGAGCTCTACCTACCTACCTGTACAGAGGTCAAGGCA 401
QY 436 AGAGACCGGCGCGCTCTTCTTCATGATCATGACGCGCTCGGGAGTCAAGGCTGATCTC 495
Db 402 AGAGACCGGCGCGCTCTTCTTCATGATCATGACGCGCTCGGGAGTCAAGGCTGATCTC 461
QY 496 AGCTGCTGATGACTGAGTCTGAAAGCTGCAAGAGAGTGAAGAGCTGACCGGCTGC 555
Db 462 AGCTGCTGATGACTGAGTCTGAAAGCTGCAAGAGAGTGAAGAGCTGACCGGCTGC 521
QY 556 TGAAGTCCAAAGATGATCTTCAATCAAGAGAGTGGGTTAAGAGACGCTGTGCGCAAGC 615
Db 522 TGAAGTCCAAAGATGATCTTCAATCAAGAGAGTGGGTTAAGAGACGCTGTGCGCAAGC 581
QY 616 ACCAGAGAGCTGTGAGAGAGCTCAAGAGAGTGTGAGAGCGGCGAGGCTCAAGC 675
Db 582 ACCAGAGAGCTGTGAGAGAGCTCAAGAGAGTGTGAGAGCGGCGAGGCTCAAGC 641
QY 676 GCTGCAAGAGAGAGACTTACAGACTGCGCATGCGCTGCGGACACAGAGTGAAGAAAG 735
Db 642 GCTGCAAGAGAGAGACTTACAGACTGCGCATGCGCTGCGGACACAGAGTGAAGAAAG 701
QY 736 GCGCGCGCTCATGCGGAAACCGTGAACCTGACGTGAGATTGACCAAGCTCAAGCAAGCC 795
Db 702 GAGCAGCACTCATGCGGAAACCGTGAACCTGACGTGAGATTGACCAAGCTCAAGCAAGCC 761
QY 796 TATGAGAGCCAGAGACAGACTGCAAGTGAAGCGCAAGACACGCTGAAGCTCAGGACG 855
Db 762 TATGAGAGCCAGAGAGACTGCAAGTGAAGCGCAAGACACGCTGAAGCTCAGGACG 821
QY 856 CCATGAGAGAGCGGCGCGACGACGAGAGCTGTGAGAGCTGACAGAGAGAGAGGCGCTGC 915
Db 822 CCATGAGAGAGCGGCGCGCTTACGACGAGAGCTGTGAGAGCTGACAGAGAGAGAGCTTGT 881
QY 916 TCCAGGCGCGGCTGACAGAGCTGAGAGCTCCGTCACAGAGGAGAGCTGACAGAGAGCA 975
Db 882 TCCAGGCGCGGCTGACAGAGCTGAGAGCTCCGTCACAGAGGAGAGCTGACAGAGAGCA 941
QY 976 GCGCTTACATCAAGTACTGAGAGAGACTGAGAGAGCGGCGCTGCGGAGACACAGAGAGC 1035
Db 942 GCGCATACATCAAGGCTGAGAGAGAGTGAAGAGTGAAGCACTGAGAGAGACACAGAGAGC 1001
QY 1036 AGGCAACACATCTTCTCTGCGGAGAGAGACTCCGCGAGGCGAGGCGGACGCTCC 1095

Dp	1002	AGGCCACGACCACTCTTCTCCCTACGAAAGAACCTCCGCCAGGCTGAAGCCCTCCGACCC	1061
Qy	1096	GGTCATGAGAGAGAGAGATGTTTCAGCTGCAGTGCCTGGCACTACGTAAAGACTCCA	1155
Dp	1062	GGTCATGAGAGAGAAAGAGATGTTTCAGAGCTGCAGTGCCTGGCTTGCGGACAGATGCCA	1121
Qy	1156	AGATGTCAAAGAGACCGCATCGAGGCCATCTCTGCTGCAGATGAGAGAGGTGCCCATTTGAC	1215
Dp	1122	AGATGTCAAAGAGACCGGATCGAGGCTATCTCTGCAGCAGATGAGAGAGTCTCCCATTTAGC	1181
Qy	1216	GGAGCCGAGACACACAATGAGAGGGGCTGTACACAGCTCCGGCCCAAGCGGCTTGAAGT	1275
Dp	1182	GGGAC-----	1186
Qy	1276	CTTCCGAGGCTCTGTTGAGTTGGGCGGCGCGGCGAGAGGCCAGAGGCACAGCTTGAGG	1335
Dp	1187	-----	1186
Qy	1336	CCCTCACTGAAGGATCGGCGCTTGCTGTCCGTCAGGCCATAGCCACGCGGAGAGACTG	1395
Dp	1187	-----CAGGCTATGACCTCAAGGAGAGACTG	1213
Qy	1396	CACGCACAGCACGCCCGGGGCTTCGAGAGAGAGACGCGCTGCGCAGACAGGTGCGGAG	1455
Dp	1214	CATGCACAGTGTGCCCCAAAGCTTTCAGGACAAAGATTAAGCTGCAAAAGCAGAGTTCAGAA	1273
Qy	1456	CTGGGCGCAGAGGGGAGTGAAGCTCAGCTCAGCTGAGGTTCCAGTGTGAGAGCGCACTACTG	1515
Dp	1274	CTGATGAGAAAGGCCGACAGAGTTGAGGTGAGCTGTCCAGACCCGAGAGGCTGATTACTG	1333
Qy	1516	GCCGTGAGAGGACAGGACTCAGGCGGAGAGAGCTGAGACGCTGATCTAGCTCCGACTG	1575
Dp	1334	GCCGCTGAGGACAGACTCAGCAGCAGACAGCAATTGGACATGCTCATCTTGAAGCTTGACTTG	1393
Qy	1576	GAAGATGAGCTCACCCAGGAGGTCCGAGAGCTTCATCTCCCCAGAGACT--GAGGAC	1632
Dp	1394	GAAAGCAGTTCCCCAGAGACCTCCAGAGAGGTTTCACTGCTCAGGACTTGAGAGAGGAGAT	1453
Qy	1633	ACCCAGCTCTCAGACAAAGGCTGCTTCCGAGCGGGGAGAGCCGAAACAGCCCTTGCA	1692
Dp	1454	GCCCAAGCTCTCAGACAAAGGCTGTCTCGACAGACAGGAGAGACCCAGACAGCCCTTGCTG	1513
Qy	1693	GCTCTGACACAGAGCAGAGTTTTGGCGAACCCCATGACGAGGCTTAGAGACGGGGAG	1753
Dp	1514	GTTCTGAAACAAGAAAGCATCTTTGGAGA--CCCATGACGGTGTCCAGACGACGAG	1570
Qy	1753	CCGCCGAGAGAGAGCGGCGGCGCTCTCAAAGAGATTTTGAAGATTCAGCAGAGAGGC	1812
Dp	1571	CCCCCGAGAGAGAGCGGCGGCGCTCTCAAAGAGAGCTTCGAGACTTACCGCAGAGAGCG	1633
Qy	1813	GCCCTCAGAGAAATGCAAGAAAGATGCGGCGCAGAGGGGAGAGAGACCGGAGAAACAACG	1872
Dp	1631	GCGCTCCGCAAGATCAGAACAGCTGGGGAACAGGGAAGAGGGGATCAAGGGAAATGACA	1690
Qy	1873	GGCAGCGCAACACCGACACTGAGGGCTTCAGCCGACAGACTTCCCGAGCGCTGCG	1933
Dp	1691	GGCAGCGCAACACCGACACCGAGGCTCTTAGAGAACACCGCCAGAGCTGAGCTGTGT	1750
Qy	1933	TGACTTGCGCTGGAACG	1949
Dp	1751	GTAAATTGAAAGGATG	1767

REFERENCE	1	Elkayyoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	Bertin, J.	
TITLE	Molecules of the card-related protein family and uses thereof	
JOURNAL	Patent: WO 0140468-A 3 07-JUN-2001;	
	Millennium Pharmaceuticals, Inc. (US)	
FEATURES	Location/Qualifiers	
source	1..1608	
	/organism="Rattus norvegicus"	
	/mol_type="Genomic DNA"	
	/db_xref="taxon:10116"	
BASE COUNT	407 a	252 t
ORIGIN	435 c	514 g

Query Match	78.0%;	Score 1045;	DB 6;	Length 1608;
Best Local Similarity	47.9%;	Pred. No. 1.6e-144;		
Matches 1370;	Conservative	0;	Mismatches 235;	Indels 154;
			Gaps	3
QY	147	ATGTGGACTACGAGAACGATGACGAGTGGTGAACGTCCTTGGAGGGCTTCCGGGTGACG	206	
Db	1	ATGTCAAGACTAAGAAATAGACGAGAGTGGTAGTGCCTCTGAGAGCTTCCGGGTGAAG	60	
QY	207	CTCACTCGGTGATGACCCCTCAAGGATACACTTACTCTGGGAGTGCMAAGGCTCG	266	
Db	61	CTATATTTCTGTCAATGACCCCTCAAGAAATCAACCTTATTTGGGCGAGTGCMAAGTCTTG	120	
QY	267	AACCTGTAGTAGAGACAGAGTGTCTCAGCAGCCCAACTGTGATTCGCAACCGAAA	326	
Db	121	AACCCGAGTAGAGAGACAGAGTGTCTCAGTACCCCAACTGTGATTCGCAACCGAAA	180	
QY	327	GTGGGTGTGTCTCTTGGACATCTCTCAGCGGACCGGCAAAAGGCTTACGTGGCTTCTTC	386	
Db	181	GTGGGTGTGTCTCTTGGACATCTCTCAGCGGACCGGCAAAAGGCTTACGTGGCTTCTTC	240	
QY	387	GAGAGCTTGGAGCTCTTACATCCCGAGGTGTAACAAGAGTCAACAGCAAGAGCCGGCC	446	
Db	241	GAGAGCTTGGAGCTCTTACATCCCTCAGTATACAGAAAGTCACTGCGCAAGAGCCAGCG	300	
QY	447	CGCGTTTCTTCATGATCATGACGCGTCCGGGGAGTCAAGCTTGACTCAGCTGTGATG	506	
Db	301	CGGTCTTCTTCATGATCATGACGCAACGATCAAGGGGAGTCCGGGCTTGAACAGCTGTGATG	360	
QY	507	ACTGAGCTCATGAACCTGCAGAAAGAGTGTGAGAGACTGACCGCGTGTGACTCCAA	566	
Db	361	ACGAGAGTCAATGAAGTGTGAGAAAGGTTGAGAGCTTGAACGCGCTTCTGAAGCTCCAG	420	
QY	567	GATGATTTCAATCAAGAGAGTGTGGGTTGAAGACAGCTGTGTGCGCAAGCACAGAGAGCT	626	
Db	421	GATGATTTCAATCAAGAGAGTGTAGGTTAAGGACAGCTTCTGTGGCAAGCACAGAGAGCG	480	
QY	627	GTGCAAGAGCTCAAGAGAGAGTGTGAGGCGGACGCGGAGCTCAAGCCTTGCAAGAG	686	
Db	481	GTGCAACGAGCTCAAGAGAGAGTGTGAGCTGTGACGTGACAGTGTGCGAGTGAAGCCCTCAAGAGAT	540	
QY	687	GAGAACTAAGACCTGGCCATATGCGCTGGCGACCAAGATGAGAGAGAGAGGGCGCGCGCTC	746	
Db	541	GAGAACTAAGACCTGGCCATATGCGCTGGCTCACTTGAATGAAGAGAGAGAGAGCACTC	600	
QY	747	ATGCGGAAACCGTGACCTGTGACGTGTGAGATTAGCAAGCTCAAGCAACAGCTCATGAAGGCC	806	
Db	601	ATGCGGAAACCGTGACCTGTGAGCTTGAAGTGAACCAAGCTCAAGGCAACAGCTCATGAAGGCA	660	
QY	807	GAGAGAGACTGCAAGTGTGAGAGGCGCAAGACACGCTGAAGCTCAAGGCAACGCCATATGAGAG	866	
Db	661	GAGAGAGACTGCAAGTGTGAGAGGCGCAAAACAACCTGAAGGCTTCCGACACGCTATATGAGACAG	720	
QY	867	CGGAGCCAGCAAGAGCTGTGTGTGAGAGCTGTGACAGCAGAGAGAGGCGCTGTCTCAGAGCCCG	926	
Db	721	CGGAGCTTACCAAGAGAGCTGTGTGTGAGAGCTGTGACAGCAGAGAGAGGACTTTGTTCAGAGCCCG	780	
QY	927	GTGCAAGAGAGCTGAGAGGCTTCCGTTCAGAGAGGAGAGAGTGTGACAGAGACAGAGCCCTTACATC	986	

```

Db      781 GTGAGAGAGTGGAGGCTCTCCGTGACAGAGGTAAGTTACACAGGATACCCATTCATC 840
Qy      987 CAGTACTGAGAGAGACCTGCGCGCAGAGCGCTGCGGAGACCAAGAGAGAGCCAAACC 1046
Db      841 CAGGTGCTGAGAGAGAGCTGGCGCTCAGGACCTGAGAGAAACACAGAGAGCGGACACACC 900
Qy      1047 ATCTTCTCCCTGCGAGAGACCTTCGCGCAGAGCGGAGCGGAGCGCTCCGCTGATGAG 1106
Db      901 ATCTTCTCCCTGAGAAAGACCTTCGCGCAGAGCGGAGCGGAGCGCTCCGCTGATGAG 960
Qy      1107 GAGAGAGAGATGTTGAGAGCTGAGAGCTGCTGAGAGCTAGTAAAGATCTCAAGATGTAAG 1166
Db      961 GAAAGAGAGATGTTGAGAGCTGAGAGCTGCTGAGAGCTAGTAAAGATGTAAG 1020
Qy      1167 GACCGATGAGAGCGCATCTGCTGCTGAGAGAGAGAGTGGCATGAGCGGAGCAGAGC 1226
Db      1021 GACCGATGAGAGCGCATCTGCTGCTGAGAGAGAGAGTGGCATGAGCGGAGC----- 1074
Qy      1227 ACAGAAATGAGAGGCTGTGACAGAGCTTCGCGCGCAGAGCGGCTTGAAGTCCGAGCC 1286
Db      1075 ----- 1074
Qy      1287 TCTGCTTGAAGTTGAGCGCGCGCGGCGAGGCGCCAGGCGCAAGCTTGGGCGCTCATGAG 1346
Db      1075 ----- 1074
Qy      1347 GGTGCGCTTGTGCTGTCTCCGTACAGGCGCATAGCCAGCGGAGAGAGTGCACGACAGCA 1406
Db      1075 -----CAGGCTATGACCTCAAGGAGAAAGTGCATGACACAGTG 1112
Qy      1407 CGCGCGGCGCGCTGAGAGAGAGAGAGCGGCTGCGAGAGAGAGTGGAGAGTGGCGAGAA 1466
Db      1113 TGCCCAAGGCTTGAAGCAAGATTAAGCTGCGAAACAGAGTTCGAACTGAGATGAGAA 1172
Qy      1467 GCGCGATGAGCTGAGAGCTGAGAGTGTTCAGTGTGAGAGCGCAGCTACTGCGCGTGAAGG 1526
Db      1173 GCGCGAGAGAGTGTGAGAGCTGAGAGTGTTCAGAGAGAGCGAGTACTGCGCGCTGAGAGG 1232
Qy      1527 CAGGCTCAGCGGAGAGAGAGCTGAGAGAGCTGTCTGAGCTCCGACTGAGAGATGAGCTC 1586
Db      1233 CAGACTCAGAGAGAGAGAGATGAGAGTGTCTGAGCTCTGAGCTTGAAGAGAGCTTC 1292
Qy      1587 ACCCAGAGAGCTCCAGAGAGCTCTCACTCCCGCAGAGACT--GAGAGACACCAAGCTTC 1643
Db      1293 CCCAGAGAGACTCCAGAGAGCTTTCACCTGCTCAGAGAGCTGAGAGAGATGCCAGGCTTC 1352
Qy      1644 AGAGAAAGGCTGCTTGCAGCGCGGAGAGAGCGGAGAGCGGAGAGCGCTTGCAGCTGAGCA 1703
Db      1353 AGAGAAAGGCTGCTTGCAGCGAGAGAGAGCGGAGAGCGGAGAGCGGAGAGCGCTTGCAGCA 1412
Qy      1704 GAGAGAGGTTTTCGAGAAACCCCATGACGAGAGCTTGAAGAGAGCGGAGAGCGGAGAGAA 1763
Db      1413 GAGAGATCTTTCGAGAG--CCATGACAGAGTCCCGAGAGAGCGGAGAGCGGAGAGAA 1469
Qy      1764 GAGAGCGGCGGCGCTCAAGAGAGATTTGAGAACTACCGAGAGAGCGGCGCTCAGAGAA 1823
Db      1470 GAGAGCGGCGGCGCTCAAGAGAGATTTGAGAACTACCGAGAGAGCGGCGCTCAGAGAA 1529
Qy      1824 GATGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
Db      1530 GATGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1589
Qy      1884 CACGAGACCTGAGGAGCTCC 1902
Db      1590 CACGAGACCTGAGGAGCTCC 1608

```

```

RESULT 10
BD150612 765 bp DNA linear PAT 17-JAN-2003
LOCUS BD150612
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD150612

```

```

VERSION BD150612.1 GI:27856370
KEYWORDS UP 2002191363-A/5455.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Ota,T., Iwoga,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
AUTHORS Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 5455 09-JUL-2002;
HEALTH RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/5455
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAZUO
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KENICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
C12N5/10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N5/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FEATURES
source FT source 1..765
Location/Qualifiers
BASE COUNT 160 a 236 c 242 g 123 t 4 others
ORIGIN
Query Match 33.3%; Score 725.4; DB 6; Length 765;
Best Local Similarity 99.0%; Pred. No. 2.2e-97;
Matches 759; Conservative 0; Mismatches 5; Indels 3; Gaps 3;
Qy 1 ATCATCAGAGAGTGCACAGAGCGTCCGCGTCTCTCTCCCTGAGAGCGGAGAGCA 60
Db 1 ATCATCAGAGAGTGCACAGAGCGTCCGCGTCTCTCTCCCTGAGAGCGGAGAGCA 60
Qy 61 TCTCCAGAGAGGCTCCGCGCGCAGAGGCTCTGAGTGTGTGTGAGTGCAGTGAAGTGTCTCTGGA 120
Db 61 TCTCCAGAGAGGCTCCGCGCGCAGAGGCTCTGAGTGTGTGTGAGTGCAGTGAAGTGTCTCTGGA 120
Qy 121 AACCCCTCAGCGCTGCTGAGAGCGCATGTGAGAGAGAGAGAGAGAGAGTGTCTGGA 180
Db 121 AACCCCTCAGCGCTGCTGAGAGCGCATGTGAGAGAGAGAGAGAGAGAGTGTCTGGA 180
Qy 181 AGCTCTGAGAGGCTTCCGAGTGAAGCTCACTCCGCTCAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 AGCTCTGAGAGGCTTCCGAGTGAAGCTCACTCCGCTCAGAGAGAGAGAGAGAGAGAGAG 240
Qy 241 CTTACCTGCGGAGAGTGCAGAGTCTGAACTGATGATGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 CTTACCTGCGGAGAGTGCAGAGTCTGAACTGATGATGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 301 CCAACTGATCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 CCAACTGATCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 GCCAGAGAGGCTACGAGTGTCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GCCAGAGAGGCTACGAGTGTCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 AGAAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 AGAAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 AGTACAGCTGACTGAGCTGTGATGACTGAGGTCATGAGAGAGAGAGAGAGAGAGAGAG 540

```

QY	188	CAACGACACTGAGGGGCTCTAGCCGACGACAGACCTTCCCCAGCCGTCGTGACTTGGACCT	1943
QY <td>293</td> <td>CACCGACACTGAGGGGCTCTAGCCGACGACAGACCTTCCCCAGCCGTCGTGACTTGGACCT</td> <td>234</td>	293	CACCGACACTGAGGGGCTCTAGCCGACGACAGACCTTCCCCAGCCGTCGTGACTTGGACCT	234
Db <td>1944</td> <td>GGAACGAGAACTCTGTCCTTGAAGGCCACGCCGACTGCTCGGGCACTTGGGGCCGTTT</td> <td>2003</td>	1944	GGAACGAGAACTCTGTCCTTGAAGGCCACGCCGACTGCTCGGGCACTTGGGGCCGTTT	2003
QY <td>233</td> <td>GGAACGAGAACTCTGTCCTTGAAGGCCACGCCGACTGCTCGGGCACTTGGGGCCGTTT</td> <td>174</td>	233	GGAACGAGAACTCTGTCCTTGAAGGCCACGCCGACTGCTCGGGCACTTGGGGCCGTTT	174
Db <td>2004</td> <td>GTTAAGGGGACACTATTTGGGGAGGCGCATGGGGGTCTCAACAACCCCATGCAAGCC</td> <td>2063</td>	2004	GTTAAGGGGACACTATTTGGGGAGGCGCATGGGGGTCTCAACAACCCCATGCAAGCC	2063
QY <td>173</td> <td>GTTAAGGGGACACTATTTGGGGAGGCGCATGGGGGTCTCAACAACCCCATGCAAGCC</td> <td>114</td>	173	GTTAAGGGGACACTATTTGGGGAGGCGCATGGGGGTCTCAACAACCCCATGCAAGCC	114
Db <td>2064</td> <td>ATCTGTAACTTCAGGATCTGTTCTGTTTCAACATGTAAACAACAATATCATGATGAT</td> <td>2123</td>	2064	ATCTGTAACTTCAGGATCTGTTCTGTTTCAACATGTAAACAACAATATCATGATGAT	2123
QY <td>113</td> <td>ATCTGTAACTTCAGGATCTGTTCTGTTTCAACATGTAAACAACAATATCATGATGAT</td> <td>54</td>	113	ATCTGTAACTTCAGGATCTGTTCTGTTTCAACATGTAAACAACAATATCATGATGAT	54
Db <td>2124</td> <td>TGTTTATGTTGTAAGAAACAAGTGGGTAATTAAGCAAGCGGTACACCCGC</td> <td>2176</td>	2124	TGTTTATGTTGTAAGAAACAAGTGGGTAATTAAGCAAGCGGTACACCCGC	2176
QY <td>53</td> <td>TGTTTATGTTGTAAGAAACAAGTGGGTAATTAAGCAAGCGGTACACCCGC</td> <td>1</td>	53	TGTTTATGTTGTAAGAAACAAGTGGGTAATTAAGCAAGCGGTACACCCGC	1

RESULT 12	AL592301/c	LOCUS	DEFINITION
	AU592301	188462 bp	DNA linear PRI 27-FEB-2002
			Human DNA sequence from clone RPI-413M3 on chromosome 9, complete

ACCESSION	sequence.
VERSION	AL592301
KEYWORDS	AL592301.14 GI:19031459
HMG.	(no specific function)

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (27-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Dunn, M.
1 (bases 1 to 188462)
Direct Submission

COMMENT

On Feb 28, 2002 this sequence version replaced 01.1813.5088. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emi: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP. Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr9>
RP11-413M1 is from the library R1C1-11.2 constructed by the group
of Plierer et al. For further details see
<http://www.chori.org/bacpac/home.htm>

<http://www.ncbi.nlm.nih.gov/ncbi/patent>
 VECTOR: pBAC3.6
 This sequence is the entire insert of clone RP11-413M3 The true

FEATURES

Location/Qualifiers

left end of clone RP11-611D20 is at 179704 in this sequence.

```

FEATURES
source
location/Qualifiers
1. .188462
/organism="Homo sapiens"

```

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="cacon:3606"

```



```

/chromosome="9"
/clone_1ib="RP1-413M3"
misc_feature 7263..7383
  /note="Sequence from overlapping clone RP13-270115
  (AL603784). Assembly confirmed by restriction digest."
  25952..26034
misc_feature 41309..41325
  /note="Sequence from overlapping clone RP13-270115
  (AL603784). Assembly confirmed by restriction digest."
  105369..105382
misc_feature 141901..141955
  /note="Sequence from overlapping clone RP13-270115
  (AL603784). Assembly confirmed by restriction digest."
  172065
misc_feature 172065
  /note="Tandem repeat. Forced join. Gap size estimated to
  be approximately 1000bp by restriction digest data."
  176494..176745
misc_feature 179220..179521
  /note="Sequence from overlapping clone RP13-270115
  (AL603784). Assembly confirmed by restriction digest."
  179220..179521
misc_feature 179220..179521
  /note="Sequence from overlapping clone RP13-270115
  (AL603784). Assembly confirmed by restriction digest."
  56455 c 54358 g 36864 t

BASE COUNT 40785 a 56455 c 54358 g 36864 t
ORIGIN

Query Match 17.9%; Score 389.8; DB 9; Length 188462;
Best Local Similarity 72.8%; Pred. No. 2.4e-48;
Matches 643; Conservative 0; Mismatches 17; Indels 223; Gaps 2;

QY 457 CCATGATCATCGACCGGTCCTCCGGGAGTCAGAGCTGACTGAGCTGATGAGTCACTGAGTCA 516
DB 14781 CCGGGCCCAACAGACGGGTCGGGAGTCAGAGCTGACTGAGTCACTGAGTCACTGAGTCA 14722
QY 517 TGAAGCTGACAGAGAGAGTGCAGAGACCTGACCGGCTGCTGAGCTCCAAAGATGATTC 576
DB 14721 TGAAGCTGACAGAGAGAGTGCAGAGACCTGACCGGCTGCTGAGCTCCAAAGATGATTC 14662
QY 577 TCAAGAGCTGCGGCTGTAAGAGACACCTGCTGCGACAGACCAAGACCGCTGTGCAGAGGC 636
DB 14661 TCAAGAGCTGCGGCTGTAAGAGACACCTGCTGCGACAGACCAAGACCGCTGTGCAGAGGC 14602
QY 637 TCAAGAGAGTGTGAGGCGCGGACGCGGAGCTCAAGCCCTGCAAGAGAGAGAACTAG 696
DB 14601 TCAAGAGAGTGTGAGGCGCGGACGCGGAGCTCAAGCCCTGCAAGAGAGAGAACTAG 14542
QY 697 ACCGCGGCAACCGGCTGCGGACCAACAGAGTGAAGAGAGGCGCGGCTCATGCGGAAAC 756
DB 14541 ACCGCGGCAACCGGCTGCGGACCAACAGAGTGAAGAGAGGCGCGGCTCATGCGGAAAC 14482
QY 757 GTGACCTGACGCTG----- 771
DB 14481 GTGACCTGACGCTGAGAGTGGCCCGCTGCCCGGAGAAACAGAGCCACCTGCGCTGGC 14422
QY 772 ----- 771
DB 14421 CTGGCGGGGCTGTGAGGCGGGGCGGTGGGGGGTGGCCCAAGGGTCTGCGGTACCGGC 14362
QY 772 ----- AGATTGACCAAGCTCAAGCACAGCTTC 797
DB 14361 TGAAGGGACAGACCAAGCTCACTGACACTTCTGACAGATTGACCAAGCTCAAGCACAGCTTC 14302
QY 798 ATGAAGGCGGAGAGAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 857
DB 14301 ATGAAGGCGGAGAGAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 14242
QY 858 ATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 917
DB 14241 ATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 14182
misc_feature

```

```

QY 918 CAGGCCCCGGTGCAGAGAGCTGAGAGCCTCCGTC----- 950
DB 14181 CAGGCCCCGGTGCAGAGAGCTGAGAGCCTCCGTCAGAGTGGGGCCGTAGAGAGAGAGAGT 14122
QY 951 -----CAG 953
DB 14121 CAGCCCAAGCAGAGCAGTGGGAGCTTCCAGCCAGAGCCATTGCTTTTGGCCCCCTTAC 14062
QY 954 GAGGGGAAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013
DB 14061 GAGGGGAAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 14002
QY 1014 GCGTGGCGGACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073
DB 14001 GCGTGGCGGACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 13942
QY 1074 CAGGCGAGGCGCCGACGCTCCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1116
DB 13941 CAGGCGAGGCGCCGACGCTCCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 13899

RESULT 13
AB086061 2031 bp mRNA linear VRT 01-MAY-2003
LOCUS Cyprinus carpio CARD mRNA for caspase recruitment domain protein,
DEFINITION complete cds.
ACCESSION AB086061
VERSION AB086061.1 GI:21326822
KEYWORDS
SOURCE Cyprinus carpio (common carp)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acanthopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE 1
  Kono,T., Sakai,T. and Sakai,M.
  Molecular cloning and expression analysis of a novel caspase
  recruitment domain protein (CARD) in common carp Cyprinus carpio L.
  Gene 309, 57-64 (2003)
  2 (bases 1 to 2031)
  Sakai,M. and Kono,T.
  Direct Submission
  Submitted (03-JUN-2002) Masahiro Sakai, Miyazaki University,
  Faculty of Agriculture, Gakuen kibandai nishi 1-1, Miyazaki,
  Miyazaki 889-2192, Japan (E-mail:m.sakai@cc.miyazaki-u.ac.jp,
  Tel:81-985-58-7219, Fax:81-985-58-7219)
FEATURES
  source
    1..2031
      Location/Qualifiers
        organism="Cyprinus carpio"
        mol_type="mRNA"
        db_xref="taxon:7962"
        /clone="PG1"
        /tissue_type="head kidney"
        /country="Japan:Miyazaki"
        1..2031
        /gene="CARD"
        99..1706
        /gene="CARD"
        /codon_start=1
        /product="caspase recruitment domain protein"
        /protein_id="BAC00527.1"
        /db_xref="GI:21326823"
        /translation="WFDPGGGEVEDEDECMARLEDYRMILIKTIEPSRIPTYRPOCK
        VISSDEEQLVNDPSLVTRRRVGMLDLIDLTGTYEAFLESLDIPDYRKITG
        KEPARVFSVLTIDTAGECGLTQIMEVEARLQCLADERRKLEVAQVABQDITROL
        QCESEILHQODRVGRIRIEERETCEEARLQDENYRLMHDITRLSEDKNCLMNRD
        IOLTEIKHSLMNAESDSKIQKKTIVLKNAMERSPDLIMOLRENDILKARQI
        LKSARKVQTLERHKUDSOSLEPRKQSOAQVOELVNDLYNLAKDILDAEELSDYRQ
        KQELBCKTLMKDMKMTDRVEDTLKQLEVIYKRDYVITREYTHLENSLNQDQ
        QYRKQIRENGERYDELQVQLFTQGEVYALHSLKRLKQKNPQVNSSESSLSPFEMKS
        QTSSESRERGERKDESSQSTSGEYVYNSKMPSEETSNANCKLKGKCNFYRKRRA
        LRTKFTDKESVQCLINDNTTSGSDTDGM"
        156..416
misc_feature

```

Query Match	17.2%	Score 374.8;	DB 5;	Length 2031;
Best Local Similarity	60.1%;	Pred. No. 8.5e-46;		
Matches 653;	Conservative 0;	Mismatches 412;	Indels 21;	Gaps 1;
Query	159	GAGAACCATGACGAGTGGCTGGAAGCTCTGGAGGCGCTCCGGGAGACGCTCACCTGGCTG	218	
Db	129	GAGAGGAGTGTGAGTGTGTGGCCGGCTGGAGACATACAGATGCTTCTCATACAGACC	188	
Qy	219	ATCGACCCCTCACCACATCACACTTACCTCGGCGAGTGCAGAGCTCTGAACCTGATGAT	278	
Db	189	ATTGAGCCCTCAAGATATACACCTTTACTGTGACAAATGTAAAGTGTGAGACGAGGAC	248	
Qy	279	GAGAGACAGTGTCTGACGACCCCAACTGTGCTATCCGCAACGGAAGTGGTGTCTC	338	
Db	249	GAAAGAACGATCTCTCAATGACCCCAAGCTGTGTATCAGCGGTAGAAAAGTTGGGATCTG	308	
Qy	339	CTGACATCTCTGACCGGACCGGCGACAAAGGCTACGTGGCTCTTCCTCGAGGCTGGAG	398	
Db	309	CTGGACATATTATCAACGAACTGGGCTTCAAGGAATGTAGAGATTCTTAGAGATTGGAG	368	
Qy	399	CTCTACTACCCGCGAGCTGTACAAAGAGTGCACAGGCAAGAGCCGCGCTCTTCTCC	458	
Db	369	CTAAGACTTCCAGATGTGTACCGCAAAATATCCGCGCAAAAGGCTCTGATGGTCTTCTCC	428	
Qy	459	ATGATCATGACGCGTCCGGGAGTACAGGCTGTACTGACTGTGATGACTGAGCTATG	518	
Db	429	GTACTTATTGACAGGCGCGGTGAATGTGGCTCACTGACTCTTAATGAGCGAGTCTCT	488	
Qy	519	AAAGCTGCAGAAAGAGTGCAGAGC-----TGACCGGCTCTGTG	557	
Db	489	CGCTTACAGAAAGCTTGCACAGAGCAAGACGAGAGACGACTCGAAGTGTCTCCGCAAGTG	548	
Qy	558	AGCTCAAAAGATGACTTATCAAGAGGTGGGGGTGAAGGACAGCTGCTCCGCAAGAC	617	
Db	549	GCGGAGCAGCTAGACACATCCGCGAGCTTGAGCTGTGTGAGGCGAGCTGCACAAACAG	608	
Qy	618	CAGAGCGTGTGCAGAGGCTCAAGAGAGTGCAGAGCCGCGAGCCGCGAGCTCAAGGC	677	
Db	609	CAGAGCCGGTGCAGCGCATCCGAGAGAGCGCGAGCCGACGCTGCGAGAGGCGCGTAAA	668	
Qy	678	TGCAGAGAGAGAACTTACGACTGTGGCCATGTGGCTCTGGCGCACACAGAGTGAAGAAAGGC	737	
Db	669	CTGAGAGACGAAATTACCGACTGTGACGACCTCGAACCGCGCTGAGGAGAGACAAAGAC	728	
Qy	738	GCGCGGCTCATGCGGAACCGTGAACCTGAGCTGAGGATTGACAGCTCAAGCACAGCTCTC	797	
Db	729	TGCGGCTCATGTGTAAACAGAGACCTCCAGCTCGAGATTGAGAAATTAAACACAGCTTA	788	
Qy	789	ATGAAGCCGAGAGACGACTGCAAGGTGAGGCGCAAGCAAGCTGMAAGCTCAAGCACGCC	857	
Db	789	ATGAATGCAAGAAAGTACATCAAAAGATCCAAACGGAAGAAAAAAGTAACTTGAAGATCG	848	
Qy	858	ATGAGACAGCGGCCCAAGCAGAGTGTGTGTGGAGCTGACGACGAGAAAGAGGCTGTCTC	917	
Db	849	ATGGAGCAGAGGCGCAAGTCTGTAGCTGTGCTGGCGATTGACAGAGAAATGACATCTCTT	908	
Qy	918	CAGGCGCCGGGTGCAGAGAGCTGAGAGCGTCCGTCAGAGAGGGAAGCTGACAGAGCAGC	977	
Db	909	AAAGCTCGCATCAGAGAGCTCAAAAGTGTCTTCAAGAGTCCAACTCTGAGGATTAAGAAA	968	
Qy	978	CCCTACATCAGAGTACTGAGAGAGACTGGCGGCGAGCGCTTCCGGGACCAACCAAGAGAG	1037	
Db	969	CTTGATTCACTCATTTAGAGAAATTCAGAGCAAAAGTCAAGACCAATACAGAGAGCTG	1028	
Qy	1038	GCGAACCACTTTCTCCCTGCGCAAGACCTTCGCGCAGAGGCGAGAGCCCGAGCTCTCCG	1097	

Db	Accession	Definition	Source
Db	1029	GTGAATGATCTCTACAACTCTAAGGAAGAACCCTACATGACGACGAAGAAGCTGAGTGATAAG	1088
Cy	1098	TGCATGAGAGAGAGAGAGATGTTTCGAGCTTCGACTGCTTGGCACTAGCTAAGAGCTCCAG	1157
Db	1089	TATCGACAGAGAGAGATGTAACCTAGAGCTGGAAGTGTATATGTTTAAAAAGAGAGCCAAA	1148
Cy	1158	ATGTAACAAGAGACCGCATCGAGGCGCATCCGCTGCAGATGAGAGAGGTGCGCATTTGAGCGG	1217
Db	1149	ATGTACCGTACCGCATGGAAGACATTTGGAAGCAGCTGGAAGAAGGTCACTCAAGAAGAAGA	1208
Cy	1218	GACCAG 1223	
Db	1209	GACGAG 1214	
RESULT 14			
LOCUS	AY135367	4085 bp mRNA linear ROD 27-OCT-2002	
DEFINITION	Mus musculus caspase recruitment domain family member 11 (Card11)		
ACCESSION	AY135367		
VERSION	AY135367.1	GI:24415470	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 4085)		
AUTHORS	Pomerantz, J. L., Denny, E. M. and Baltimore, D.		
TITLE	CARD11 mediates factor-specific activation of NF-kappaB by the T cell receptor complex		
JOURNAL	EMBO J. 21 (19), 5184-5194 (2002)		
MEDLINE	22240460		
PUBMED	12356734		
REFERENCE	2 (bases 1 to 4085)		
AUTHORS	Pomerantz, J. L., Denny, E. M. and Baltimore, D.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JUL-2002) Biology, California Institute of Technology, MC 147-75, 1200 E. California Blvd., Pasadena, CA 91125, USA		
FEATURES			
source	1..4085	location/Qualifiers	
gene	1..4085	organism="Mus musculus"	
CDs	1..4085	mol_type="mRNA"	
	1..4085	/db_xref="taxon:10090"	
	1..4085	/tissue_type="thymus"	
	1..4085	/gene="Card11"	
	218..3697	/gene="Card11"	
	218..3697	/note="signaling protein"	
	218..3697	/codon_start=1	
	218..3697	/product="caspase recruitment domain family member 11"	
	218..3697	/protein_id="AA010150.1"	
	218..3697	/db_xref="GI:24415471"	
	218..3697	/translation="MPGGGPRMDDYMETLCKDEEALNDVNCNRMISRYINPAKTLTLYROCKVITDEDEEDVNAAPMLPSKINAGRLDLILHTKGQGVAFLESLEFYPEEYKLVITGKEPTRRFSTIIIVEEGHEGLTHLNMNEVTLQQGVAKDLQRCELAKRQLEDEKQSLIRVEELTFQERYKKEERDSYNDELVKVDQVYNILAMRAYQSEENMMAKTSIPKMSQKSEFQALMRATYGHEDDTDSPESSRELPTVSSFSKQPKRSRSISITLAPPEINDSVIRCKEDAPHRSTVEEDNDSQPDALDLIDENHERYSPGPSIHSSSHOSBGLDADYDLQVYMLRKRSLSBEPREPSVTSGAHVGTGZIVQHTLINDGGLTQTLTLGNARGSFTHSVKPSLAPRGLRGGHLLBEGCIRGERQSPVLDATKREARWTLQRCSGGLITLHKVNHGGRYKLKEMEDGLTSDGSFYIRLNTNISQLDACSLSLKCDVYVHLITQODRHEWLCAKRVPTFDQDITGTIPSYRAQQLLVKLRVYHAKGNREDAVHHTLRNLTLOPEMLSTSDPSRPSRLPRASPFGLQGVSRSENNYKRNMSNRVRLIGSGSPGISRSLSLDTKLLTEHHELDPENLSRLTLIPSVIV	

AHCEHRRRPLFTPLAKTIVOKLINSGAMEFTICKSDIVTRDFLEKQETITLY
 SEKHNTEPCTIPANIEBAVAKNKGICRDLICKVPIVILLIVSEKNI
 KRRRLPRREHEEFRLVRCKELKELMLPCILVATVEKMSVSEELLRLVKDIVE
 EORRTIWDVDDQJ"

BASE COUNT 1113 a 1137 c 1148 g 687 t

Query Match 17.2%; Score 373.8; DB 10; Length 4085;
 Best Local Similarity 60.6%; Pred. No. 1.1e-45;
 Matches 665; Conservative 0; Mismatches 402; Indels 30; Gaps 2;

157 ACAGAGACGATGACGAGTGTGGAAGCTCTGAGAGGCTTCGCGGTGAGCTCACTCGG 216
 264 AGATGAGAGAGAGGCGCTTATGGATATACGTGAATGCAACCGGCACTGTGAGCCGT 323
 217 TCATCGACCCCTGACGATCAACCTTACCTGCGGAGTGCAGAGTCTTGAACCTGTATG 276
 324 ACATCAACCCCGCAAGCTCACCCCTACTGCGCAGTGCAGAGTCAATGATGAGCAG 383
 277 ATGAGAGCAGGTGTCTCAGCAGCCCACTGTCTATCCGCAACGGAAGTGGGTGTGC 336
 384 ATGAGAGCAGGTGTCTCAGCAGCCCACTGTCTATGATCAACCGTGCAGGCCGAT 443
 337 TCCTGACATCTCTGACGCGGACCGGCCACAGGGCTTACGTCCTTCTGAGAGCTGG 396
 444 TGTGGACATTTCTTACACCAAGGACAAAGGGCTATGTGTCTTCTGAGAGCTGG 503
 397 AGCTTACTACCCGACGCTGTACAGAGGTCAAGGACAGGACCGGCGCGCTTCT 456
 504 AGTTTACTCTCCAGAACTTACAACTGTGTGCTGGAAGGAAACCCACCGGAGTTCT 563
 457 CCATGATCATCGACGGTCCGGGAGTCAAGCTGCTGATGATCACTGAGTCA 516
 564 CCACCATGTGTGTGAGAGAGGCCATGAGGGCTTCAACACTTCTGTGATGAAGAGTCA 623
 517 TGAAGCTGCAGAGAGGTGCAAGAC-----CTGACCGGCGCTGC 555
 624 TCAAACTGCAGCAGAGTGAAGGACCTTGAAGCGCTGTGAGCTGTGGCCAGT 683
 556 TGAGCTCCAAAGATGACTTATCAAGAGAGTGGGGTGAAGGACACCTGTGGCGAAGC 615
 684 CCGGCACTGTGAGATGAGAGAGAGAGTGAAGCTGATACGGGTGAGAGTGTGACT 743
 616 ACCAGAGCCTGTGACAGAGCTCAAGAGAGTGCAGAGCGCGGACCGGACCTCAAGC 675
 744 TCCAGAGCCTATCTACAAATGAGAGAGAGCGGAGCAGCTACATGACAGCTGTCA 803
 676 GCTGCAAGAGAGAACTAGACCTTGGCCATGCGCTGTGGGACCAAGATGAGAGAGG 735
 804 AGGTCAAGAGAGCACTACTACACTTATGCGCTACGCGCTACGCGCTCACTGAGAGAAA 863
 736 GCGCGCGCTCATGCGGACCTGAGAGCTGTGAGATGATGACGCTCAAGAGAGC 795
 864 ACATGGCGGTGATGAGAGAGCGCGACCTCCAACTCGAGATGACAGCTCAACACCGAG 923
 796 TCATGAGAGCGGAGAGAGCTGCAAGGTGAGAGCGCAAGCAACGCTGAGTCAAGCAAG 855
 924 TGAACAAGATGAGAGAGAGATGCAAGTGAAGAAATCACTCCCTCAAGCTCAAGAAAG 983
 856 CCATGAGAGCAGCGCCAGCAGAGAGCTGTGAGAGCTGCAGAGAGAGAGAGCCTTCTC 915
 984 ACATCCAGAACCGGCGCAGAGAGAGAGAGTCTGTGAGCTGAGAGCGGAGAGAAATGATGC 1043
 916 TCCAGGCGCGGTGACAGAGCTGAGAGCTTCCCTCCAGAGAGGGAAG-----CTGG 966
 1044 TGAAGAGAAATTCAGAGAGCTGAGTCACTATCCAGAGCTGCGCAGAGAGCCTCCTG 1103
 967 ACAGAGACAGCCCTTACATCAAGTACTGAGAGAGAGCTGCGCAGAGAGCCTTGGGAGCC 1026
 1104 ACTCAGACAAAGGCGATCTTGAACATCTGTGAACATGACCGGAAAGAGGCGCTTGAAGAGCC 1163
 1027 ACAGAGAGAGGCGCAACACATCTTCTCCTGGCGAAGAGACCTCCGCGAGAGGAGCC 1086

1164 GGCAGGAATGATGACAAATAATTACACTTACAGAGAGAGTCCCGAGCGAGAGC 1223
 1087 GAGCGCTCCGGGATGAGAGAGAGAGAGATGTTGAGCTGACAGTCCGACACTAGCTA 1146
 1224 TGGGAGATGAGTACTGAGAGAGAGAGAGAGAGCTGGAATCAAGTGTCAACCTTGGGGA 1283
 1147 AGAATCCAGATGATCAAGAGAGCGCATGAGGCGATCTGCTGAGATGAGAGAGTGC 1206
 1284 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1343
 1207 CCATTGAGCGGAGACCAAG 1223
 1344 AGCGGAGCGGAGACCAAG 1360

RESULT 15
 AX154573
 LOCUS AX154573 3441 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 12 from Patent WO0140468.
 ACCESSION AX154573
 VERSION AX154573.1 GI:14536166
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1
 AUTHORS Bertin, J.
 TITLE Molecules of the card-related protein family and uses thereof
 JOURNAL Patent: WO 0140468-A 12 07-JUN-2001;
 Millennium Pharmaceuticals, Inc. (US)
 FEATURES
 source 1..3441
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 868 a 999 c 1025 g 549 t

ORIGIN

Query Match 17.1%; Score 372.2; DB 6; Length 3441;
 Best Local Similarity 60.5%; Pred. No. 1.9e-45;
 Matches 564; Conservative 0; Mismatches 403; Indels 30; Gaps 2;

157 ACAGAGACGATGACGAGTGTGGAAGCTCTGAGAGGCTTCGCGGTGAGCTCACTCGG 216
 264 AGATGAGAGAGAGGCGCTTATGGATATACGTGAATGCAACCGGCACTGTGAGCCGT 323
 217 TCATCGACCCCTGACGATCAACCTTACCTGCGGAGTGCAGAGTCTTGAACCTGTATG 276
 324 ACATCAACCCCGCAAGCTCACCCCTACTGCGCAGTGCAGAGTCAATGATGAGCAG 383
 277 ATGAGAGCAGGTGTCTCAGCAGCCCACTGTCTATCCGCAACGGAAGTGGGTGTGC 336
 384 ATGAGAGCAGGTGTCTCAGCAGCCCACTGTCTATGATCAACCGTGCAGGCCGAT 443
 337 TCCTGACATCTCTGACGCGGACCGGCCACAGGGCTTACGTCCTTCTGAGAGCTGG 396
 444 TGTGGACATTTCTTACACCAAGGACAAAGGGCTATGTGTCTTCTGAGAGCTGG 503
 397 AGCTTACTACCCGACGCTGTACAGAGGTCAAGGACAGGACCGGCGCGCTTCT 456
 504 AGTTTACTCTCCAGAACTTACAACTGTGTGCTGGAAGGAAACCCACCGGAGTTCT 563
 457 CCATGATCATCGACGGTCCGGGAGTCAAGCTGCTGATGATCACTGAGTCA 516
 564 CCACCATGTGTGTGAGAGAGGCCATGAGGGCTTCAACACTTCTGTGATGAAGAGTCA 623
 517 TGAAGCTGCAGAGAGGTGCAAGAC-----CTGACCGGCGCTGC 555
 624 TCAAACTGCAGCAGAGTGAAGGACCTTGAAGCGCTGTGAGCTGTGGCCAGT 683
 556 TGAGCTCCAAAGATGACTTATCAAGAGAGTGGGGTGAAGGACACCTGTGGCGAAGC 615
 684 CCGGCACTGTGAGATGAGAGAGAGAGTGAAGCTGATACGGGTGAGAGTGTGACT 743
 616 ACCAGAGCCTGTGACAGAGCTCAAGAGAGTGCAGAGCGCGGACCGGACCTCAAGC 675
 744 TCCAGAGCCTATCTACAAATGAGAGAGAGCGGAGCAGCTACATGACAGCTGTCA 803
 676 GCTGCAAGAGAGAACTAGACCTTGGCCATGCGCTGTGGGACCAAGATGAGAGAGG 735
 804 AGGTCAAGAGAGCACTACTACACTTATGCGCTACGCGCTACGCGCTCACTGAGAGAAA 863
 736 GCGCGCGCTCATGCGGACCTGAGAGCTGTGAGATGATGACGCTCAAGAGAGC 795
 864 ACATGGCGGTGATGAGAGAGCGCGACCTCCAACTCGAGATGACAGCTCAACACCGAG 923
 796 TCATGAGAGCGGAGAGAGCTGCAAGGTGAGAGCGCAAGCAACGCTGAGTCAAGCAAG 855
 924 TGAACAAGATGAGAGAGAGATGCAAGTGAAGAAATCACTCCCTCAAGCTCAAGAAAG 983
 856 CCATGAGAGCAGCGCCAGCAGAGAGCTGTGAGAGCTGCAGAGAGAGAGAGCCTTCTC 915
 984 ACATCCAGAACCGGCGCAGAGAGAGAGAGTCTGTGAGCTGAGAGCGGAGAGAAATGATGC 1043
 916 TCCAGGCGCGGTGACAGAGCTGAGAGCTTCCCTCCAGAGAGGGAAG-----CTGG 966
 1044 TGAAGAGAAATTCAGAGAGCTGAGTCACTATCCAGAGCTGCGCAGAGAGCCTCCTG 1103
 967 ACAGAGACAGCCCTTACATCAAGTACTGAGAGAGAGCTGCGCAGAGAGCCTTGGGAGCC 1026
 1104 ACTCAGACAAAGGCGATCTTGAACATCTGTGAACATGACCGGAAAGAGGCGCTTGAAGAGCC 1163
 1027 ACAGAGAGAGGCGCAACACATCTTCTCCTGGCGAAGAGACCTCCGCGAGAGGAGCC 1086

Db 446 TGGGAGAGCTGGAGGATGAGAAAGACAGATGACGGCTGACGGCGTGGAGCTGCTAACCT 505
QY 616 ACCAGAGAGGCTGTGCGAGAGGCTCAAGGAGAGGTGGAGGCGGCAAGCGGCGAGCTCAAGC 675
Db 506 TCCAGGAGCGGTACTGCAAGATGAGAGAGAGGGGAGCACTACAAATGAGAGGCTGTCA 565
QY 676 GTTGCAGAGAGGAGAACTACGACCTTGGCCATGCGCTTGGCGACACAGAGTGAAGAGAGG 735
Db 566 AGGTGAGAGAGCAACACTACACTTAGCCATGGCTACGACACAGCTCACTGAGAGAGAG 625
QY 736 GCGCCGCGCTCATGCGGAAACGTTGACCTGACGTGAGATTGACCAAGCTCAAGCAAGCC 795
Db 626 ACATGCGCGGTCAATGAGAGAGCGGAGACTCCAACTCGAGATGATCAGCTAAAGCAACGGT 685
QY 796 TCATGAGAGCGGAGAGCACTGCAAGGTGAGAGGCAAGCAACAGCTGAAGCTCAGGACG 855
Db 686 TGAATTAAGATGAGAGAGGATGTAGCTGAGAGAAATCAGTCTTAAACTGAAGAAATG 745
QY 856 CCATGAGAGAGCGGCGGCGGAGAGAGCTGTGTGGAGGCTGACAGAGAGAGAGGCGCTTGC 915
Db 746 ACATTGAAATTCGGCCCAAGAGAGAGCAAGTTCTGGAACCTGGAACGCGGAGAAATGAATGC 805
QY 916 TCCAGGCGCGGTGCAAGAGCTGAGAGGCTCCGTCCAGAGAGGGA-----GCTGC 966
Db 806 TGAAGACCAAAACAGAGAGCTCAGTCCATCATCCAGGCGGGAAGCGGAGCTTGCAG 865
QY 967 ACAGAGAGAGCGCCCTTACATCCAGGTACTGAGAGAGAGCTGGCGGCAAGCGCTTGCAGGACC 1026
Db 866 ACTCAGACAAAGGCGCATCTGTGACATCTTGAACACGACGCAAGAGAGGCGCTTGAAGACA 925
QY 1027 ACCAGAGAGAGGCGCAACACCATCTTCTCCCTGGCGCAAGAGCTCCGCGCAGGCGAGGCGCC 1086
Db 926 GGCAGAGAGCTGTCAACAGAGATCTACACCTGCAAGAGAGGCGCCGCGCAGGCAAGAGAGC 985
QY 1087 GAGCGCTCCGCTGATGAGAGAGAGAGATGTTGAGCTGACAGTGCCTTGCACCTACGTA 1146
Db 986 TGCAGACCAAGTACTGAG 1045
QY 1147 AGGACTTCAAGATGTACAG 1206
Db 1046 AGGACTGTGAATGTACAG 1105
QY 1207 CCATTGAGCGGAGAGAG 1223
Db 1106 AGCGGAGCGGAGAGAG 1122

Search completed: February 23, 2004, 13:30:53
Job time : 7918 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 09:51:40 ; Search time 620 Seconds

(without alignments)
9474.157 Million cell updates/sec

Title: US-10-032-159A-19

Perfect score: 2176

Sequence: 1 atccatcaggaagtgccacagg.....aaacagcagcggctgaccgcg 2176

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

25: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2176	100.0	2176	22	AAH18321	Human cDNA sequencin
2	2176	100.0	2176	25	ABX11432	DNA encoding caspase
3	1746	80.2	2098	22	AA505387	Human caspase recr
4	1746	80.2	2098	24	ABA00332	Human CARD-9 cDNA
5	1060.2	48.7	1879	22	AA505386	Rat caspase recrui
6	1060.2	48.7	1879	24	ABA00331	Rat CARD-9 cDNA
7	725.4	33.3	765	22	AAH08620	Human cDNA clone (
8	398	18.3	413	22	AAH13540	Human cDNA clone (

9	375.8	17.3	3744	25	ABX11430 Human caspase recr
10	372.2	17.1	4275	22	AA505389 Human caspase recr
11	372.2	17.1	4276	24	ABA00334 Human CARD-11 cDNA
12	367.4	16.9	1663	25	ACC50413 Human secreted pro
13	367.4	16.9	1663	25	ABZ71230 Human secreted pro
14	355.4	16.3	1687	22	AA505585 Human secreted pro
15	355.4	16.3	1687	22	ACC50719 Human secreted pro
16	355.4	16.3	1687	25	ABZ71397 Secreted protein-e
17	348.4	16.0	524	21	ABZ75276 Human ORF831
18	348.4	16.0	524	24	ABN25534 Human ORF polynuc
19	273.6	12.6	881	25	ABX11433 Human CARD-10X exp
20	273.6	12.6	828	21	AACT6941 Human ORF2496
21	264	12.1	3948	24	AA598203 DNA encoding plako
22	264	12.1	3949	22	AA505388 Human caspase recr
23	264	12.1	3949	24	ABA00333 Human CARD-10 cDNA
24	239.4	11.0	446	24	ABN25029 Human ORF polynuc
25	232.6	10.7	734	25	ABX11434 Chicken CARD-10X e
26	175.4	8.1	711	24	AA598201 DNA encoding plako
27	166.6	7.7	570	22	AA505620 Human secreted pro
28	166.6	7.7	570	25	ACC50720 Human secreted pro
29	166.6	7.7	570	25	ABZ71398 Secreted protein-e
30	148.6	6.8	446	24	ABN25029 Human ORF polynuc
31	137.8	6.3	3931	22	AAZ13447 Human caspase recr
32	132.8	6.1	9551	20	AAZ22301 cDNA encoding a hu
33	101	4.6	3489	21	AAA30290 Kaposi's sarcoma-a
34	101	4.6	3489	22	AAF82901 Nucleotide sequenc
35	101	4.6	3489	24	ABA93487 Kaposi's sarcoma-a
36	101	4.6	32207	20	AAV73805 KSHV LTR DNA (nucl
37	101	4.6	137507	19	AAV19941 KSHV long unique c
38	100.6	4.6	799	19	AAV55831 Nucleotide sequenc
39	100.6	4.6	1926	21	AA50254 Epstein Barr virus
40	100.6	4.6	1826	22	AAF82902 EBV tethering prot
41	100.6	4.6	2580	21	AAV74544 Nucleotide sequenc
42	100.6	4.6	2580	24	AA164275 Epstein-Barr virus
43	100.6	4.6	5452	20	AAZ90923 Anti-sense strand
44	100.6	4.6	8705	20	AAZ23778 Vector phuntle DN
45	100.6	4.6	9600	19	AAV21683 Vector plasmid pcm

ALIGNMENTS

RESULT 1					
AAH18321					
ID	AAH18321	standard;	cDNA;	2176 BP.	
XX					
AC	AAH18321;				
XX					
DT	26-JUN-2001	(first entry)			
XX					
DE	Human cDNA sequence SEQ ID NO:18327.				
KW	Human, primer, detection; diagnosis; antisense therapy; gene therapy; ss.				
XX					
OS	Homo sapiens.				
XX					
PN	EP1074617-A2.				
XX					
PD	07-FEB-2001.				
XX					
PF	28-JUL-2000;	2000EP-0116126.			
XX					
PR	28-JUL-1999;	99JP-0248036.			
PR	27-AUG-1999;	99JP-0300253.			
PR	11-JAN-2000;	2000JP-0118776.			
PR	02-MAY-2000;	2000JP-0183767.			
PR	09-JUN-2000;	2000JP-0241899.			
XX					
PA	(HELT-) HELIX RES INST.				
XX					
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;				
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;				

DR MPI; 2001-318749/34.
XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 18327; 2537pp + CD ROM; English.
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2176 BP; 464 A; 657 C; 734 G; 321 T; 0 other;
Query Match 100.0%; Score 2176; DB 22; Length 2176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCATCAGAGAGTCCACAGGCGTCCGCGTCTCTCCCTCCCTGACCCCGGAGCA 60
Db 1 ATCATCAGAGAGTCCACAGGCGTCCGCGTCTCTCTCTCTCCCTGACCCCGGAGCA 60
QY 61 TCTCCAGAGGCTCCGCGGCCAGGCTCTTGTGTGTCTGAGTGCAGGTGGCTCTGGA 120
Db 61 TCTCCAGAGGCTCCGCGGCCAGGCTCTTGTGTGTCTGAGTGCAGGTGGCTCTGGA 120
QY 121 AGACCTCTACGCTGCTGCTGAGGCACTGTGAGACTGAGAGAGTGAAGAGTGGTGA 180
Db 121 AGACCTCTACGCTGCTGCTGAGGCACTGTGAGACTGAGAGAGTGAAGAGTGGTGA 180
QY 181 AGCGCTCGAGAGGCTTCGCGGTGAGCGCTCAGCTGAGTATGAGCCCTTACGATCAGC 240
Db 181 AGCGCTCGAGAGGCTTCGCGGTGAGCGCTCAGCTGAGTATGAGCCCTTACGATCAGC 240
QY 241 CTTAACCTGCGGAGTGAAGTCTTGAACCTTGAATGATGAGAGCAGAGTGTGACGACC 300
Db 241 CTTAACCTGCGGAGTGAAGTCTTGAACCTTGAATGATGAGAGCAGAGTGTGACGACC 300
QY 241 CTTAACCTGCGGAGTGAAGTCTTGAACCTTGAATGATGAGAGCAGAGTGTGACGACC 300
Db 241 CTTAACCTGCGGAGTGAAGTCTTGAACCTTGAATGATGAGAGCAGAGTGTGACGACC 300
QY 301 CCAACTGTGATCCTCCGCAAGAGTGGTGTGCTCTGAGACATCTCTGACGACCG 360
Db 301 CCAACTGTGATCCTCCGCAAGAGTGGTGTGCTCTGAGACATCTCTGACGACCG 360
QY 361 GCCACAGAGGCTAGTGGCTCTTCTCAGAGCCTGAGAGCTTACTACCCGAGTGTACA 420
Db 361 GCCACAGAGGCTAGTGGCTCTTCTCAGAGCCTGAGAGCTTACTACCCGAGTGTACA 420
QY 421 AGAAGTCAAGAGAGAGAGCGGCGCGCTTCTCATGATCATGACGCTCCGAGG 480
Db 421 AGAAGTCAAGAGAGAGAGCGGCGCGCTTCTCATGATCATGACGCTCCGAGG 480
QY 481 AGTCAGGCTGACTAGTGTGTGATGATGAGTCAAGTCAAGAGAGTGTGACG 540
Db 481 AGTCAGGCTGACTAGTGTGTGATGATGAGTCAAGTCAAGAGAGTGTGACG 540

QY 541 ACTGACCGCGCTGCTGAGCTCCAAAGTACCTTCATCAAGAGAGTCCGAGTGAAGACA 600
Db 541 ACTGACCGCGCTGCTGAGCTCCAAAGTACCTTCATCAAGAGAGTCCGAGTGAAGACA 600
QY 601 GCTGCTCGCAAGACCAAGAGCGTGTGACAGAGCTTCAGAGAGAGTGCAGGCGGCA 660
Db 601 GCTGCTCGCAAGACCAAGAGCGTGTGACAGAGCTTCAGAGAGAGTGCAGGCGGCA 660
QY 661 GCTGCTCGCAAGACCAAGAGCGTGTGACAGAGCTTCAGAGAGAGTGCAGGCGGCA 660
Db 661 GCTGCTCGCAAGACCAAGAGCGTGTGACAGAGCTTCAGAGAGAGTGCAGGCGGCA 660
QY 721 AGAGTGAAGAGAGAGAGCGCGCTCATGCGGAAACCGTGAAGCTGAGTGAAGTGAAC 780
Db 721 AGAGTGAAGAGAGAGAGCGCGCTCATGCGGAAACCGTGAAGCTGAGTGAAGTGAAC 780
QY 781 AGCTCAGACAGAGCTCTCATGAGAGCGGCGAGAGAGCTGCAAGTGAAGCAAGC 840
Db 781 AGCTCAGACAGAGCTCTCATGAGAGCGGCGAGAGAGCTGCAAGTGAAGCAAGC 840
QY 841 TGAAGTCAAG 900
Db 841 TGAAGTCAAG 900
QY 901 AGGAG 960
Db 901 AGGAG 960
QY 961 AGCTGAG 1020
Db 961 AGCTGAG 1020
QY 1021 GGGAG 1080
Db 1021 GGGAG 1080
QY 1081 AGGAG 1140
Db 1081 AGGAG 1140
QY 1141 TACGTGAAG 1200
Db 1141 TACGTGAAG 1200
QY 1201 AGGTGAG 1260
Db 1201 AGGTGAG 1260
QY 1261 CAG 1320
Db 1261 CAG 1320
QY 1321 AGGAG 1380
Db 1321 AGGAG 1380
QY 1381 AGGAG 1440
Db 1381 AGGAG 1440
QY 1441 AGGAG 1500
Db 1441 AGGAG 1500
QY 1501 GAGGAG 1560
Db 1501 GAGGAG 1560
QY 1561 CTGAGCTCGAG 1620
Db 1561 CTGAGCTCGAG 1620

QY 1621 GACCTGAGGACACCCAGCTTCTCAGACAAAGGCTGCTTCCGCGCGGGGAGACCCGAAA 1680
 DB 1621 GACCTGAGGACACCCAGCTTCTCAGACAAAGGCTGCTTCCGCGCGGGGAGACCCGAAA 1680
 QY 1681 CAGGCTTTGAGAGTCTGCAACAGAGCAGGTTTTGGGAAACCCCAAGAGTTCAGAGGCTTG 1740
 DB 1681 CAGGCTTTGAGAGTCTGCAACAGAGCAGGTTTTGGGAAACCCCAAGAGTTCAGAGGCTTG 1740
 QY 1741 AGCAGCGGGAGCGCGCCGAGAGAGAGCGCGGCGCTCAAGAGAGTTCAGAGGCTTG 1800
 DB 1741 AGCAGCGGGAGCGCGCCGAGAGAGAGCGCGGCGCTCAAGAGAGTTCAGAGGCTTG 1800
 QY 1801 CGCAGAGAGCGCGCCCTCAGAGAGAGTTCAGAGAGAGTTCAGAGAGAGTTCAGAGAG 1860
 DB 1801 CGCAGAGAGCGCGCCCTCAGAGAGAGTTCAGAGAGAGTTCAGAGAGAGTTCAGAGAG 1860
 QY 1861 GAGAAACACACAGGAG 1920
 DB 1861 GAGAAACACACAGGAG 1920
 QY 1921 CCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 DB 1921 CCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 QY 1981 ACTGCGGGGAGTGGGGCGGCTTGTAAAGCGGCACTATTTGGAGAGGCAAGCGGGTG 2040
 DB 1981 ACTGCGGGGAGTGGGGCGGCTTGTAAAGCGGCACTATTTGGAGAGGCAAGCGGGTG 2040
 QY 2041 CTCACACACCCCATGACACAGGCACTGTGTAACTTGAAGATCTGTTTTCACCATG 2100
 DB 2041 CTCACACACCCCATGACACAGGCACTGTGTAACTTGAAGATCTGTTTTCACCATG 2100
 QY 2101 TAAACACAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 DB 2101 TAAACACAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 QY 2161 AGCAGCGGCTGACCCCGC 2176
 DB 2161 AGCAGCGGCTGACCCCGC 2176

RESULT 2
 ABX11432 standard; DNA; 2176 BP.
 ID ABX11432 standard; DNA; 2176 BP.
 AC XX
 ABX11432;
 XX
 DT 09-MAY-2003 (first entry)
 XX
 XX
 XX DNA encoding caspase recruitment domain containing protein, CARD-10X.
 XX
 XX CARD; caspase recruitment domain; cancer; glioma; carcinoma; adenocarcinoma;
 KW cytokine receptor signaling; apoptosis; cell adhesion; inflammation;
 KW CARD-containing polypeptide associated disorder; sarcoma; melanoma; ds;
 KW hamatoma; leukemia; lymphoma; keratinocyte hyperplasia; neoplasia;
 KW keloid; benign prostatic hyperplasia; inflammatory hyperplasia; fibrosis;
 KW restenosis; allergy; arthritis; lupus; Sjogren's syndrome; sepsis; gene;
 KW Crohn's disease; ulcerative colitis; graft versus host disease; stroke;
 KW abnormal cell death disease; myocardial infarction; heart failure;
 KW neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV;
 KW CARD-10X; caspase activator; caspase inhibitor.
 XX
 XX OS
 XX Unidentified.
 XX
 XX Key Location/Qualifiers
 FT 147..1247
 FT /tag= a
 FT /product= "CARD-10X"
 FT 180..395
 FT /tag= b
 FT /note= "Encodes caspase recruitment domain (CARD).
 FT Specifically claimed in claim 2"
 FT misc_feature 606..1037

FT /*tag= c
 FT /note= "Encodes filament domain. Specifically claimed in
 FT claim 2"
 FT
 PN US2002164703-A1.
 XX
 PD 07-NOV-2002.
 XX
 XX 19-DEC-2001; 2001US-0032159.
 PF
 PR 21-DEC-2000; 2000US-257457P.
 XX
 PA (PAWL/) PAWLOWSKI K.
 PA (REED/) REED J C.
 PA (GODZ/) GODZIK A.
 XX
 PI Pawlowski K, Reed JC, Godzik A;
 XX
 XX MPI; 2003-288137/28.
 DR P-PSDB; AEG76060.
 DR
 XX
 PT New isolated CARD-containing nucleic acids, useful for the diagnosis
 PT and treatment of disorders with aberrant expression or activity of the
 PT CARD-containing polypeptide, such as cancer, stroke, arthritis, heart
 PT failure and AIDS
 XX
 PS Disclosure; Fig 4; 34pp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule encoding a
 CC caspase recruitment domain (CARD) containing polypeptide. CARD containing
 CC polypeptides are involved in apoptosis (as caspase activators and caspase
 CC inhibitors), cell adhesion, inflammation and cytokine receptor
 CC signaling. The methods and compositions of the present invention are
 CC useful for the diagnosis and treatment of disorders associated with the
 CC aberrant expression or activity of the CARD containing polypeptide such
 CC as cancer, glioma, carcinoma, adenocarcinoma, sarcoma, melanoma, keloid,
 CC hamatoma, leukemia, lymphoma, keratinocyte hyperplasia, neoplasia,
 CC benign prostatic hyperplasia, inflammatory hyperplasia, fibrosis,
 CC restenosis, allergy, arthritis, inflammatory diseases such as arthritis, lupus,
 CC Sjogren's syndrome, Crohn's disease, ulcerative colitis, graft versus
 CC host disease, sepsis, abnormal cell death diseases such as stroke,
 CC myocardial infarction, heart failure, neurodegenerative diseases like
 CC Parkinson's disease and Alzheimer's disease, and HIV infection. The
 CC present sequence represents DNA encoding the caspase recruitment domain
 CC containing protein, CARD-10X.
 CC
 XX
 XX Sequence 2176 BP; 464 A; 657 C; 734 G; 321 T; 0 other;
 SQ

Query Match 100.0%; Score 2176; DB 25; Length 2176;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATAGGAGATGACACAGGCTCCGCGGTGCTCCCTCCCTGAGAGCCCGGAGAGA 60
 DB 1 ATCATAGGAGATGACACAGGCTCCGCGGTGCTCCCTCCCTGAGAGCCCGGAGAGA 60
 QY 61 TCTCCAGAGAGGCTCCGCGGCTCCGCGGTGCTCCCTCCCTGAGAGAGTGTGCTCTGGA 120
 DB 61 TCTCCAGAGAGGCTCCGCGGCTCCGCGGTGCTCCCTCCCTGAGAGAGTGTGCTCTGGA 120
 QY 121 AGACCTGAGGCTCCGCGGTGCTCCGCGGTGCTCCCTCCCTGAGAGAGTGTGCTCTGGA 180
 DB 121 AGACCTGAGGCTCCGCGGTGCTCCGCGGTGCTCCCTCCCTGAGAGAGTGTGCTCTGGA 180
 QY 181 AGCTCTGAGAGGCTCCGCGGTGCTCCGCGGTGCTCCCTCCCTGAGAGAGTGTGCTCTGGA 240
 DB 181 AGCTCTGAGAGGCTCCGCGGTGCTCCGCGGTGCTCCCTCCCTGAGAGAGTGTGCTCTGGA 240
 QY 241 CTTACTGCGGAGAGTCAAGATCTGGAACCTGATATGAGAGAGAGTGTGCTCAAGAGAGC 300
 DB 241 CTTACTGCGGAGAGTCAAGATCTGGAACCTGATATGAGAGAGAGTGTGCTCAAGAGAGC 300
 QY 301 CCAACTGTGATCCGCAAGAGAGAGTGTGTGTCTGTGAGACATCTGACAGGAGCG 360

Dp	301	CCAACCTGTGTCATCCGCMAAGGAAAGTGGGTGTGCTCTGGAGATCTCTGAGATACCTCCGAGGGACCG	360
Qy	361	GCCACAAGGGCTACGTGGCTTCTCTCGAAGCCTGGAGCTTCTACTACCCGAGCTGTACA	420
Dp	361	GCCACAAGGGCTACGTGGCTTCTCTCGAAGCCTGGAGCTTCTACTACCCGAGCTGTACA	420
Qy	421	AGAAAGTTCACAGGCAAGAGGCCGGCCCGCGCTCTCTCCATGATATGACGCGCTCCGGGG	480
Dp	421	AGAAAGTTCACAGGCAAGAGGCCGGCCCGCGCTCTCTCCATGATATGACGCGCTCCGGGG	480
Qy	481	AGTACAGGCTTACCTCAGCTGCCTGTGATGACTGATGAGCTCATGAAAGCTCAGAAAGAGGTGCAAG	540
Dp	481	AGTACAGGCTTACCTCAGCTGCCTGTGATGACTGATGAGCTCATGAAAGCTCAGAAAGAGGTGCAAG	540
Qy	541	ACCTGACCCGCTGCTGAGCTCCAAAGATGACTTCATCAAGAGACTCGGGGTGAAGACA	600
Dp	541	ACCTGACCCGCTGCTGAGCTCCAAAGATGACTTCATCAAGAGACTCGGGGTGAAGACA	600
Qy	601	GCTGTGCTGCGAAGCACCAAGAGAGGTGTGCGAGAGGCTTCAGAGAGAGTGTGAGAGCCGCGCA	660
Dp	601	GCTGTGCTGCGAAGCACCAAGAGAGGTGTGCGAGAGGCTTCAGAGAGAGTGTGAGAGCCGCGCA	660
Qy	661	GCCTGAGCTCAAGGGCTGCAAGAGAGGAACTTCGACTGGCCATGGCTGGCGAGCC	720
Dp	661	GCCTGAGCTCAAGGGCTGCAAGAGAGGAACTTCGACTGGCCATGGCTGGCGAGCC	720
Qy	721	AGAGTGAAGAGAAAGGGCGCCGCGCTCATGCGGAAACCGTGAACCTTCAGCTGAGATTGACC	780
Dp	721	AGAGTGAAGAGAAAGGGCGCCGCGCTCATGCGGAAACCGTGAACCTTCAGCTGAGATTGACC	780
Qy	781	AGCTCAAGCACAGCTCTCATGAAAGCCGAGAGACGACTGCAAGTGTGAGCGCACACACGC	840
Dp	781	AGCTCAAGCACAGCTCTCATGAAAGCCGAGAGACGACTGCAAGTGTGAGCGCACACACGC	840
Qy	841	TGAAGCTCAGGCAAGCCCATGGAAGAGCGGCCCAACACAGAGCTGTGTGGAGAGTGTGACG	900
Dp	841	TGAAGCTCAGGCAAGCCCATGGAAGAGCGGCCCAACACAGAGCTGTGTGGAGAGTGTGACG	900
Qy	901	AGGAGAAAGGCTCTCTCCAGGCTCCGGGTGCGAGAGCTGAGAGCTTCGCTCCAGAGAGGGGA	960
Dp	901	AGGAGAAAGGCTCTCTCTCCAGGCTCCGGGTGCGAGAGCTGAGAGCTTCGCTCCAGAGAGGGGA	960
Qy	961	AGCTGGAAGAGAGCAAGCCCTTACATTCAGAGTACTGGAAGAGAACTGGCGGAGGCGCTGC	1020
Dp	961	AGCTGGAAGAGAGCAAGCCCTTACATTCAGAGTACTGGAAGAGAACTGGCGGAGGCGCTGC	1020
Qy	1021	GGGACATCAAGAGAGCAAGCCCTTACATTCAGAGTACTGGAAGAGAACTGGCGGAGGCG	1080
Dp	1021	GGGACATCAAGAGAGCAAGCCCTTACATTCAGAGTACTGGAAGAGAACTGGCGGAGGCG	1080
Qy	1081	AGGCCCCAGCGCTTCGGGTGCAATGAGAGAGAGAGATGTTGAGTGTGACGTCTGGGAC	1140
Dp	1081	AGGCCCCAGCGCTTCGGGTGCAATGAGAGAGAGAGATGTTGAGTGTGACGTCTGGGAC	1140
Qy	1141	TACGTAAAGACTCCAAAGATGTACAAAGGACCGCATCGAGGCCATCTGTGTCAGATGGAAG	1200
Dp	1141	TACGTAAAGACTCCAAAGATGTACAAAGGACCGCATCGAGGCCATCTGTGTCAGATGGAAG	1200
Qy	1201	AGGTGTGCAATTGAGGTGGGACCAAGAGACACAAATGGAAGGGGTGTGATCAAGCTTCGGGC	1260
Dp	1201	AGGTGTGCAATTGAGGTGGGACCAAGAGACACAAATGGAAGGGGTGTGATCAAGCTTCGGGC	1260
Qy	1261	CGAGGGCTTACAGCTCCGAGAGCTTCGCTTGAAGTGTGGAGCGGCGGAGAGGAGCC	1320
Dp	1261	CGAGGGCTTACAGCTCCGAGAGCTTCGCTTGAAGTGTGGAGCGGCGGAGAGGAGCC	1320
Qy	1321	AGGGCAAGCTTGGGGCTCTCATGAGAGGTGGGCTTGTGCTGTCCCTCCAGAGCATAGCC	1380
Dp	1321	AGGGCAAGCTTGGGGCTCTCATGAGAGGTGGGCTTGTGCTGTCCCTCCAGAGCATAGCC	1380
Qy	1381	ACGGGGAGAGCTTGCACGCAACGACGCGCGGGGCTTGCAGAGAGAGAGAGCGCTGTGCGC	1440
Dp	1381	ACGGGGAGAGCTTGCACGCAACGACGCGCGGGGCTTGCAGAGAGAGAGAGCGCTGTGCGC	1440

	Db	1381	ACGGGCGGAGAGCTGACGACAGCAAGCCGCGGGGGCTGCGAGGAGAGACGCGCTGCGC	1440
Qy	1441	AAGCAGGTGGCGGAGCTGGCGGAGAAAGCCGATGAGCTGCAGCTGCAGGTGTTCCAGTGT	1500	
Db	1441	AAGCAGGTGGCGGAGCTGGCGGAGAAAGCCGATGAGCTGCAGCTGCAGGTGTTCCAGTGT	1500	
Qy	1501	GAGGCGGAGCTGCTGGCCGTGGAAGGAGAGCTCAGGCGGAGCAGCTGAGAGCCCTGCTC	1560	
Db	1501	GAGGCGGAGCTGCTGGCCGTGGAAGGAGAGCTCAGGCGGAGCAGCTGAGAGCCCTGCTC	1560	
Qy	1561	CTGAGCTCCGACCTGGAAGATGCGTCAACCAAGAGGTCCAGAGAGCTTCACTCCCCAG	1620	
Db	1561	CTGAGCTCCGACCTGGAAGATGCGTCAACCAAGAGGTCCAGAGAGCTTCACTCCCCAG	1620	
Qy	1621	GACCTGGAAGGACACCCAGCTCTCAGACAAAGGCTGCTTGCCTGGCGGGGGAGCCCGAAA	1680	
Db	1621	GACCTGGAAGGACACCCAGCTCTCAGACAAAGGCTGCTTGCCTGGCGGGGGAGCCCGAAA	1680	
Qy	1681	CAGCCCTTTGAGCTCTGCAACAGAGACAGGTTTTCGGAAACCCCACTGACGAGGCTTG	1740	
Db	1681	CAGCCCTTTGAGCTCTGCAACAGAGACAGGTTTTCGGAAACCCCACTGACGAGGCTTG	1740	
Qy	1741	AGCAGCGGAGCGCCCGCGAGAGAGAGCGGCGCGCTCAAAAGAGTTTGAAGATAC	1800	
Db	1741	AGCAGCGGAGCGCCCGCGAGAGAGAGCGGCGCGCTCAAAAGAGTTTGAAGATAC	1800	
Qy	1801	CGCAGGAAGCGCGCTCTCAGGAGATGACAAAGATGCGCGCAGGCGGAGAGAGACCGG	1860	
Db	1801	CGCAGGAAGCGCGCTCTCAGGAGATGACAAAGATGCGCGCAGGCGGAGAGAGACCGG	1860	
Qy	1861	GAGAAACACACGGGCGAGCGACACACCGCACCTAGAGGCTTCTAGCCGCGAGACACTTCC	1920	
Db	1861	GAGAAACACACGGGCGAGCGACACACCGCACCTAGAGGCTTCTAGCCGCGAGACACTTCC	1920	
Qy	1921	CCGAGCGGCTGCTGACTTGGCTGGAACGAGAAATCTGTGCTCTGAAAGGCCGAGCGG	1980	
Db	1921	CCGAGCGGCTGCTGACTTGGCTGGAACGAGAAATCTGTGCTCTGAAAGGCCGAGCGG	1980	
Qy	1981	ACTGCGCGGACATTGGGGCCGTTTGTAAAGCGGACCTCATTTTGGGAGAGGCCAGTGGG	2040	
Db	1981	ACTGCGCGGACATTGGGGCCGTTTGTAAAGCGGACCTCATTTTGGGAGAGGCCAGTGGG	2040	
Qy	2041	CTCACCAACCCCATATGACACAGCCCATCTGTGTAACTTCAAGATCTGTGTTTCAACATG	2100	
Db	2041	CTCACCAACCCCATATGACACAGCCCATCTGTGTAACTTCAAGATCTGTGTTTCAACATG	2100	
Qy	2101	TAAACACAATATACATGATGATGTGTTAGTGTAGAAACACAGCTGCGTAATATAAC	2160	
Db	2101	TAAACACAATATACATGATGATGTGTTAGTGTAGAAACACAGCTGCGTAATATAAC	2160	
Qy	2161	AGCACGGGTGACCCCGC 2176		
Db	2161	AGCACGGGTGACCCCGC 2176		
RESULT 3				
AA505387				
ID	AA505387	standard, cDNA, 2098 BP.		
XX	AA505387;			
AC				
XX				
DT	12-SEP-2001	(first entry)		
XX				
DE		Human caspase recruitment domain, CARD-9 cDNA sequence.		
KM		Human, caspase recruitment domain; CARD-9; Bcl-10; Nf-kappaB.		
KW		apoptosis; hyperproliferative disorder; autoimmune; neurological;		
XX		inflammatory disorder; viral infection; stress-related response; ss.		
OS		Homo sapiens.		
XX				
Key		Location/Qualifiers		
FT	CDS	144..1754		


```

Db      1218 -----CAGGCCATAGCCACGCGGAGAGCTGCACGCAAG 1253
QY      1405 CACGCCCGGGGCTGACAGAGAGAGCGGCTGCGCAACAGAGTGGGGAG 1464
Db      1254 CACGCCCGGGGCTGACAGAGAGAGCGGCTGCGCAACAGAGTGGGGAG 1313
QY      1465 AAGGCGGATGAGTGCAGCTGCAGGTGTTCAAGTGAAGCGCACTACTGAC 1524
Db      1314 AAGGCGGATGAGTGCAGCTGCAGGTGTTCAAGTGAAGCGCACTACTGAC 1373
QY      1525 GCGAGCTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1584
Db      1374 GCGAGCTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1433
QY      1585 TCACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1644
Db      1434 TCACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1493
QY      1645 GACAAAGGCTGCTTGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1704
Db      1494 GACAAAGGCTGCTTGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1553
QY      1705 GACAGAGTTTGGGGAACCCCATGAACGAGCTGAGAGAGAGAGAGAGAG 1764
Db      1554 GACAGAGTTTGGGGAACCCCATGAACGAGCTGAGAGAGAGAGAGAGAG 1613
QY      1765 GAGCGCGGCGCTCAAGAGAGTTTGAAGATCAACGAGAGAGAGAGAGAG 1824
Db      1614 GAGCGCGGCGCTCAAGAGAGTTTGAAGATCAACGAGAGAGAGAGAGAG 1673
QY      1825 ATGCAAGAAAGATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1884
Db      1674 ATGCAAGAAAGATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1733
QY      1885 ACCGACACTGAGGAGCTCTAGCCGCA----- 1910
Db      1734 ACCGACACTGAGGAGCTCTAGCCGCAAGAGAGAGAGAGAGAGAGAGAG 1793
QY      1911 -----GCAAGTTCCTCCGAGCCGTCGCT 1933
Db      1794 CCGGCGCTGCGACCCCGGGGCTGCGAGCGCCCTGGGGGAGAGAGAGAGAG 1853
QY      1934 GACTTGGCTGGAACGAGAGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAG 1993
Db      1854 GACTTGGCTGGAACGAGAGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAG 1913
QY      1994 GGGGCGCTTGTGAAGCGGACATCTTTGCGAGAGAGAGAGAGAGAGAGAG 2053
Db      1914 GGGGCGCTTGTGAAGCGGACATCTTTGCGAGAGAGAGAGAGAGAGAGAG 1973
QY      2054 TGCAACGCGCATCTGTACTTACAGATCTGTCTTCACTGATGAACACATAC 2113
Db      1974 TGCAACGCGCATCTGTACTTACAGATCTGTCTTCACTGATGAACACATAC 2033
QY      2114 ATGATCATCTGTATTAGTGT-AGAAAACACAGCTGCGTAATTAACAGAG 2172
Db      2034 ATGATCATCTGTATTAGTGT-AGAAAACACAGCTGCGTAATTAACAGAG 2093
QY      2173 CCGC 2176
Db      2094 CCGC 2097

```

```

KW      Gene, rat; human; caspase recruitment domain; CARD-9; CARD-10;
KW      CARD-11; apoptosis; inflammation; cell growth; cell death;
KW      lymphocyte activation; cancer; melanoma; autoimmune disease;
KW      arthritis; neurological disorder; Alzheimer's disease; ss.
OS      Homo sapiens.
FH      Key Location/Qualifiers
FT      CDS 144..1754
FT      /tag= a
FT      /product= "CARD-9"
FN      WO200270652-A2.
PD      12-SEP-2002.
PF      28-FEB-2002; 2002WO-US06147.
PR      02-MAR-2001; 2001US-0798412.
PA      (MILL-) MILLENNIUM PHARM INC.
PI      Bertin J;
PI      WPI; 2002-698749/75.
DR      P-PSDB; AAG79553.
XX      CARD-9, CARD-10 or CARD-11 polypeptides and polymucleotides, useful for
XX      treating disorders associated with inappropriate apoptosis or
XX      lymphocyte activation, e.g. cancer
XX      Disclosure; Fig 5; 151pp; English.
PS      This sequence encodes human caspase recruitment domain (CARD)-9.
XX      CARD proteins play roles in apoptotic and inflammatory signaling
XX      pathways. CARD-9, -10 and -11 participate in the network of
XX      interactions that modulate caspase activity. They are thought to be
XX      useful as modulating agents for regulating a variety of cellular
XX      processes including cell growth and cell death. CARD proteins and
XX      nucleic acids are useful for treating a disorder associated with
XX      inappropriate apoptosis or lymphocyte activation or for diagnosing
XX      subjects having or that are at risk of developing a disorder associated
XX      with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such
XX      as cancer e.g. melanoma, autoimmune disorders e.g. arthritis, or
XX      neurological disorders e.g. Alzheimer's disease.
SQ      Sequence 2098 BP; 455 A; 644 C; 702 G; 297 T; 0 other;
Query Match 80.2%; Score 1746; DB 24; Length 2098;
Best Local Similarity 89.9%; Pred. No. 4.5e-295;
Matches 1999; Conservative 0; Mismatches 5; Indels 220; Gaps 3;
QY      25 CCGCGTGTCTTCTCCCTCCCTGAGCGCGGAGAGATCTCCAGAGGCTCGCGGCCAG 84
Db      22 CCGCGGCTCTCTCTCTCTGAGCGCGGAGAGATCTCCAGAGGCTCGCGGCCAG 81
QY      85 GCTCTGTGTGTCTGCAAGTGAAGTGTCTCTGGAAGACCTTCAAGCTGCTGTGAG 144
Db      82 GCTCTGTGTGTCTGCAAGTGAAGTGTCTCTGGAAGACCTTCAAGCTGCTGTGAG 141
QY      145 CCATGTGCACTACGAGAACGATGACGAGTGTGGAAGCTCTTGAGAGGCTTCCGGGTGA 204
Db      142 CCATGTGCACTACGAGAACGATGACGAGTGTGGAAGCTCTTGAGAGGCTTCCGGGTGA 201
QY      205 CGCTCACTCGGTATTCAGACCTCTCAAGCATACACTTACTGGGGAGAGGCAAGTCC 264
Db      202 CGCTCACTCGGTATTCAGACCTCTCAAGCATACACTTACTGGGGAGAGGCAAGTCC 261
QY      265 TGAACCTGATGATGAGAGAGAGAGTGTCAAGGACCCCAACCTGTGATCCGCAAGCA 324
Db      262 TGAACCTGATGATGAGAGAGAGTGTCAAGGACCCCAACCTGTGATCCGCAAGCA 321
QY      325 AAGTGGTGTGCTCTGACATCTGACCGGACCGGACCAAGGCTAAGTGGCTTCC 384

```

Db 322 AACTGGGTGTGCTCTGAGCATCTGTCAGCGAGCCGGCCAAAGGGCTTACGTGCTTTC 381
 Qy 385 TCAGAGAGCTGAGAGCTCTACTACCCGACAGCTGTACAAGAGGTCAAGAGCCAAAGAGCCGG 444
 Db 382 TCAGAGAGCTGAGAGCTCTACTACCCGACAGCTGTACAAGAGGTCAAGAGCCAAAGAGCCGG 441
 Qy 445 CCGGCTCTTCTTCATGATTCATGAGCGCTCCGGGAGGTCAAGCTTCACTGAGCTTGTGA 504
 Db 442 CCGGCTCTTCTTCATGATTCATGAGCGCTCCGGGAGGTCAAGCTTCACTGAGCTTGTGA 501
 Qy 505 TGACTAGAGTCAATGAAGCTGACAGAGAGGTGACAGACTGACCGGCTGTGAGTCCA 564
 Db 502 TGACTAGAGTCAATGAAGCTGACAGAGAGGTGACAGACTGACCGGCTGTGAGTCCA 561
 Qy 565 AAGATGACTTCAATCAAGAGAGCTCGGGGTGAAGGACAGCTGCGGAGCAAGCAAGAGAGC 624
 Db 562 AAGATGACTTCAATCAAGAGAGCTCGGGGTGAAGGACAGCTGCGGAGCAAGCAAGAGAGC 621
 Qy 625 GTGTGACAGAGCTCAAGAGAGAGTGCAGAGCCGGCAGCCGAGCTCAAGCGCTGTGAAG 684
 Db 622 GTGTGACAGAGCTCAAGAGAGAGTGCAGAGCCGGCAGCCGAGCTCAAGCGCTGTGAAG 681
 Qy 685 AGAGGAACTACGACTGTGCGCAGTGCCTGTGCGCAGCAAGAGTGAAGAAAGGCGCGCGC 744
 Db 682 AGAGGAACTACGACTGTGCGCAGTGCCTGTGCGCAGCAAGAGTGAAGAAAGGCGCGCGC 741
 Qy 745 TCATGCGGAACCGTACCTGACCTGACCTGTGAGATTGACCAAGCTCAAGCTTATTAAG 804
 Db 742 TCATGCGGAACCGTACCTGACCTGACCTGTGAGATTGACCAAGCTTATTAAG 801
 Qy 805 CCGAGAGACGACTGCAAGGTGAGAGCGACAGACAGCTGAAGCTCAAGAGCCGATGAGAGC 864
 Db 802 CCGAGAGACGACTGCAAGGTGAGAGCGACAGACAGCTGAAGCTCAAGAGCCGATGAGAGC 861
 Qy 865 AGGAGCCAGACGAGAGCTGTGAGGAGCTGTGAGAGAGAGAGAGCCCTGTCCAGAGCC 924
 Db 862 AGGAGCCAGACGAGAGCTGTGAGGAGCTGTGAGAGAGAGAGAGCCCTGTCCAGAGCC 921
 Qy 925 GGGTGCAGAGAGCTGAGAGCTTCCGTCCAGAGAGGAGAGCTGACAGAGAGAGCCCTTACA 984
 Db 922 GGGTGCAGAGAGCTGAGAGCTTCCGTCCAGAGAGGAGAGCTGACAGAGAGAGCCCTTACA 981
 Qy 985 TCCAGTACTGAGAGAGAGTGTGCGCAGAGCTGTGCGGAGACCAACAGAGAGAGCCCAACA 1044
 Db 982 TCCAGTACTGAGAGAGAGTGTGCGCAGAGCTGTGCGGAGACCAACAGAGAGAGCCCAACA 1041
 Qy 1045 CCATCTTCTCCCTGCGCAAGAGACTTCCGCGAGAGGCGGAGCCGAGCGCTCCGAGTGAAG 1104
 Db 1042 CCATCTTCTCCCTGCGCAAGAGACTTCCGCGAGAGGCGGAGCCGAGCGCTCCGAGTGAAG 1101
 Qy 1105 AGAGGAGAGAGATGTTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1164
 Db 1102 AGAGGAGAGAGATGTTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1161
 Qy 1165 AGAGCCGCATGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1224
 Db 1162 AGAGCCGCATGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1217
 Qy 1225 GCACACAATGAGAGAGGCTGTGACCAAGCTTCCGCGCCAGCGGCTTGAAGTCTCCGAG 1284
 Db 1218 ----- 1217
 Qy 1285 CCTCTGCTTGAAGTTGGCGGCGCGGCGGAGAGGCGCAAGAGCTTGGGGCTCTCACTG 1344
 Db 1218 ----- 1217
 Qy 1345 AGGGTGGCTTTGTGTCTCCGTCAGGCTTACGACGCGGAGAGAGTGTGACGACAG 1404
 Db 1218 -----CAGGCCATTAGCCACGCGGAGAGAGTGTGACGACAG 1253
 Qy 1405 CACGCCCGGGGCTGTGACAGAGAGAGAGCGGCTGCGCAAGAGAGTGTGCGGAGCTTGGCGAG 1464

Db 1254 CACGCCCGGGGCTGTGACAGAGAGAGAGCGGCTGCGCAGAGAGTGTGCGGAGCTGTGCGAG 1313
 Qy 1465 AAGGCGATGAGCTGTGACAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1524
 Db 1314 AAGGCGATGAGCTGTGACAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1373
 Qy 1525 GGCAGAGCTCAAGCGGCGAGAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1584
 Db 1374 GGCAGAGCTCAAGCGGCGAGAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1433
 Qy 1585 TCACCAGAGAGTCCAGAGAGCTTCACTCCCGCAGAGCTGTGAGAGTGTGAGAGTGTGAGAG 1644
 Db 1434 TCACCAGAGAGTCCAGAGAGCTTCACTCCCGCAGAGCTGTGAGAGTGTGAGAGTGTGAGAG 1493
 Qy 1645 GACAAAGCTGTGCTGCGGCGGAGAGAGCCGAAACAGAGCTTGTGAGCTTGTGACACAG 1704
 Db 1494 GACAAAGCTGTGCTGCGGCGGAGAGAGCCGAAACAGAGCTTGTGAGCTTGTGACACAG 1553
 Qy 1705 GAGCAGTTTTTGTGCGGAACCCCAATGACGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 1784
 Db 1554 GAGCAGTTTTTGTGCGGAACCCCAATGACGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 1613
 Qy 1785 GAGCGGCGGCGCTTCAAGAGAGTTTTGAGACTTACGAGAGAGAGCGGCTTCAAGAGAG 1824
 Db 1614 GAGCGGCGGCGCTTCAAGAGAGTTTTGAGACTTACGAGAGAGAGCGGCTTCAAGAGAG 1673
 Qy 1825 ATGCAGAAAGATGTGCGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1884
 Db 1674 ATGCAGAAAGATGTGCGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1733
 Qy 1885 ACCGACACTGAGAGGCTCTTACGCGCA ----- 1910
 Db 1734 ACCGACACTGAGAGGCTCTTACGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1793
 Qy 1911 -----GAGACTTCCCGAGCGGTGCT 1933
 Db 1794 CCGGCTGTGACACCGGAGGAGTGTGCGAGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1853
 Qy 1934 GACTTGGCTGTGAGAGAGAGATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1993
 Db 1854 GACTTGGCTGTGAGAGAGAGATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913
 Qy 1994 GGGGCGGTTTTTAAAGCGGCACTCATTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2053
 Db 1914 GGGGCGGTTTTTAAAGCGGCACTCATTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1973
 Qy 2054 TGCACAGCGCATCTGTGTAACCTTCAAGATCTGTGTTTCAACATGTAACACACATAC 2113
 Db 1974 TGCACAGCGCATCTGTGTAACCTTCAAGATCTGTGTTTCAACATGTAACACACATAC 2033
 Qy 2114 ATGATGACTTGTATTAGTGT-AGAAAACACAGCTGCGTAATTAACAGCAGGAGTAC 2172
 Db 2034 ATGATGACTTGTATTAGTGTAAAGAAAACACAGCTGCGTAATTAACAGCAGGAGTAC 2093
 Qy 2173 CCGC 2176
 Db 2094 CCGC 2097

RESULT 5

AAS05386
 ID AAS05386 standard; cDNA; 1879 BP.

AC AAS05386;
 XX

DT 12-SEP-2001 (first entry)

XX Rat caspase recruitment domain, CARD-9 cDNA sequence.

XX Rat; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB;

KW apoptosis; hyperproliferative disorder; autoimmune; neurological;

KW inflammatory disorder; viral infection; stress-related response; ss.

XX	Rattus sp.	
XX	Key	Location/Qualifiers
FT	CDS	113..1723
FT		/tag= a
FT		/product= "CARD-9"
FT		/note= "ORF is specifically claimed"
XX		
XX	W0200140468-A2.	
PN		
PD	07-JUN-2001.	
XX		
PF	01-DEC-2000; 2000WO-US32716.	
DR		
XX		
PR	03-DEC-1999; 99US-0168780.	
XX		
PR	18-FEB-2000; 2000US-0507533.	
XX		
PR	25-FEB-2000; 2000US-0513904.	
XX		
PR	10-OCT-2000; 2000US-0685791.	
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
P1	Bertin J;	
XX		
XX	WPI; 2001-367809/38.	
DR	P-PsDB; AAU01204.	
XX		
PT	Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10,	
PT	CARD-11, useful as targets for therapy, as immunogens, and in screening	
PT	and detection assays -	
XX		
PS	Claim 2; Fig 1A-1B; 145pp; English.	
CC	The present sequence encoding for novel rat caspase recruitment	
CC	domain, CARD-9 is isolated from a rat neuronal cDNA library. Also	
CC	described are novel human sequences for CARD-9, CARD-10 and CARD-11	
CC	(AAU01205-AAU01207). CARD-9, CARD-10 and CARD-11 interact with Bcl-10	
CC	which is thought to activate nuclear factor (NF)-kappaB and apoptosis.	
CC	The sequences of the invention can be used for treating a disorder	
CC	associated with abnormal levels of apoptosis by modulating the	
CC	expression or activity of CARD-9, CARD-10, or CARD-11. They can be	
CC	used for the treatment of hyperproliferative disorders (e.g. cancer),	
CC	autoimmune disorders (e.g. systemic lupus erythematosus), neurological	
CC	disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g.	
CC	Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide,	
CC	polynucleotide and an antibody which selectively binds to CARD can be	
CC	used in screening and detection assays (e.g. chromosomal mapping, tissue	
CC	typing), predictive medicine (prognostic assays, monitoring clinical	
CC	trials, and therapy (treatment and prophylaxis). The CARD polypeptide may	
CC	be used to screen for drugs that bind to and/or modulate it. CARD	
CC	sequences are potential targets for regulating inflammation, cancer,	
CC	NF-kappaB signaling, stress-related response and apoptosis in human	
CC	disease. A host cell containing a polynucleotide encoding CARD can be	
CC	used to create transgenic animals.	
SX	Sequence 1879 BP; 496 A; 503 C; 578 G; 302 T; 0 other;	
QY		
D5		
Query Match	48.7%; Score 1060.2; DB 22; Length 1879;	
Best Local Similarity	76.2%; Pred. No. 1.1e-175;	
Matches 1431; Conservative	0; Mismatches 288; Indels 158; Gaps	4
QY		
D5		
76	GCGGCCGACGGCTTCGTGTGTGTGTGCAGTGCAGATGGCTCTCTGGAGAACCCTCAGCTTCG	135
46	GTGCCCATGAGCCACGACCACTCCACTGCGAGTGCTGCCACAAGAACCTCGA-----GC	101
136	CTGCTGAGGCGCATTGTGCGACTACGAGAAGAGAGAGAGTGGTGAACGTCCTGAGAGGCT	195
102	CTACAGAGACATGTAGACTATGAAAATGACACAGATGCTGGAATGCCCTCGAGAGCT	161
196	TCCGGTGAAGCTCACCTCGGTATCGACCCCTCAAGCATCACCTTAACCTCGGCACT	255
162	TCCGGTGAAGCTAACTCTGTATTTAGACCCCTCAAGATACACACCTTATCTGCGCACT	221
256	GCAAGTCTCTGAACCTGATGATGAGAGCAGGTGCTACGACGCCCAACCTGCTGATCC	315

Db	222	GCAAAGTCTGAACCCCGAATGATGAGAGAGAGTGTCTAGTGAACCCCAACCTTGTCATCC	281
Qy	316	GCAAAAGGAAAGTGGGTGTGCTCTGGACAATCCTGACAGGAGAACCCGCAACAGGGCTAGC	375
Db	282	GCAAGCGGAAAGTGGGTGTGCTCTGGACAATCCTGACAGGAGAGGCAACAGGGCTTAGC	341
Qy	376	TGGCTTCCCTCAAGAGCTGGAGCTCTACTACCCGACGCTGTACAAAGAAAGTCAACAGCA	435
Db	342	TGGCTTTTCTTGAAGTCTGGAACCTTACACCCCTCAGTTATACAGAAAGTCACTGGCA	401
Qy	436	AGGAGCCGACCCGCTCTTCTCCATGATCATGCAACGCTCCGGGAGTCAAGGCTTACCTC	495
Db	402	AGGAGCCAGCGGCTCTTCTCCATGATCATGCAACCATCAAGGAGTCCGGGCTTAGC	461
Qy	496	AGCTGCTGATGACTGAGGTCAATGAAGTGTGAAAGAGTGCAGGACCTTGAACCGCCCTGC	555
Db	462	AGCTGCTGATGACAAGAGTCAATGAAGTGTGAAAGAGTTCAGGACCTTGAACCGCCCTTC	521
Qy	556	TGAGCTCCAAAGATGACTTCATCAAGAGAGTGGGGGTGAAGACAGGCTCTCTCCGACAGC	615
Db	522	TGAGCTCCAAAGATGACTTCATCAAGAGAGTGGGGGTGAAGACAGGCTCTCTCCGACAGC	581
Qy	616	ACCAGAGCTGTGTGCAGAGGCTCAAGAGAGAGTGCAGAGCCGACCGGAGCTCAAGC	675
Db	582	ACCAGAGCGGGTGCAGCGGCTCAAGAGAGAGTGTGAGCTGACAGAGTGCAGAGCTGAAGC	641
Qy	676	GCTGCAGAGAGAGAACTTACGACTGTGCCATGTGCCCTGTGGCGCACAGAGTGAAGAGAGG	735
Db	642	GCTCAAGAGATGAGAACTTACGACTGTGCCCATGTGCCCTGTGGCGTCACTGAGTGAAGAGAGG	701
Qy	736	GCGCCGGGCTCATGCCGGAACCGTGAACCTGACGCTGAGATTGACCAAGCTCAAGACAGCC	795
Db	702	GAGAGACTCATGTGCGAACCCTGAACCTTGAAGCTTGAGTGAACAGCTCAAGGACAGCC	761
Qy	796	TCATGAAGCCGAGAGAGCACTGCAAGGTGAGAGCGCAACAGCTGMACTGAGGACGC	855
Db	762	TCATGAAGGCAAGAGATGACTGCAAGGTGAGAGCGCAACAGCTGMACTGAGGACGC	821
Qy	856	CCATGAGACAGCGGCCCAAGCCAGAGAGTGTGTGTGGAGCTTGCACAGCAGAGAAAGGCTTGC	915
Db	822	CCATGAGACAGCGGCTTAGCCAGGAGCTGTGTGTGGAGCTTGCACAGCAGAGAAAGGCACTTGT	881
Qy	916	TTCAGAGCCCGGTGCAGAGAGCTGGAAGCCCTCCGTCCAGAGAGGGGAACTGGAACAAGAGCA	975
Db	882	TGCAGGCCCGGGTGCAGAGAGCTTGAAGGTCTTCCGTGCAGAGAGGGTAACTTACACAGGATA	941
Qy	976	GCCCCATCATCAGATTACTGGAGAGAGACTGGCGCAGAGCGCTTCCGGGAAACCAACAGAGGC	1035
Db	942	GCCCCATCATCAGATTACTGGAGAGAGACTGGCGCTCAGGCACTGTCCAGGAACAACAGAGGC	1001
Qy	1036	AGGCCAAACCATTTCTTCCTGTGCGAAGACCTTCGTCAGAGGCGAAGCCCGGACGCTTCC	1095
Db	1002	AGGCCAGACCATTTCTTCCTTACGAAAGACCTTCGTCAGAGGCGTTCGACCTTCCGCAACC	1061
Qy	1096	GGTGCATGAGAGAAAGAGATGTTTCCAGTCTCACTGTGCACTTGGCACTAGTAAAGACTCCA	1155
Db	1062	GGTGCATGAGAGAAAGAGATGTTTCCAGTCTCACTGTGCACTTGGCACTTGGCAAGAGATGCA	1121
Qy	1156	AGATGTACAGAGACCGCATTCGAGGCACTCTGTGCAGATGAGAGAGGTCCCATTTGAGC	1215
Db	1122	AGATGTACAGAGACCGCATTCGAGGCTTCTGTGCAGAGATGAGAGAGTCTTCCATTGAGC	1181
Qy	1216	GGGACCAAGAGACAATAATGAGAGGGGCTGTGACCAAGCCTCCGCGCCAGCGCTTGACGT	1275
Db	1182	GGGAC-----	1186
Qy	1276	CCTCCGAGCCTCTGCTTGAATTTGGGCTGGCCGGCCGAGGAGCCCAAGGCAAGCTTGGGG	1335
Db	1187	-----	1186
Qy	1336	CCCTCACTGAGAGGTGAGGCTTGTGTGCTGCCGTGACAGGCTATAGCCAGCGGAGAGAGCTG	1395


```

Db      642 GCTGCAAGATGAGAACTACGACCTGCGCCCTGCGCTCACTGAGTGAAGAAAG 701
Qy      736 GCGCCGCGCTCATGCGGGAACCGTGACTGAGCTGGAGATTGACCAAGCTCAAGCAAGCC 795
Db      702 GAGCAGCACTCATGCGGAAACCGTGACTTGAAGCTTGAAGCTCAAGCTCAAGCAAGCC 761
Qy      796 TCATGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855
Db      762 TCATGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 821
Qy      856 CCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 915
Db      822 CCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
Qy      916 TCCAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 975
Db      882 TGACGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 941
Qy      976 GCGCCCTCATCTCAGAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1035
Db      942 GCGCATATCATCTCAGAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
Qy      1036 AGGCGCAACACCATCTTCTCCCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1095
Db      1002 AGGCGCAACACCATCTTCTCCCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1061
Qy      1096 GGTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1155
Db      1062 GGTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1121
Qy      1156 AGATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1215
Db      1122 AGATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1181
Qy      1216 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1275
Db      1182 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1146
Qy      1276 CCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1335
Db      1187 ----- 1186
Qy      1336 CCTCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1395
Db      1187 -----CAGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1213
Qy      1396 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1455
Db      1214 CATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1273
Qy      1456 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1515
Db      1274 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1333
Qy      1516 GCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1575
Db      1334 GCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1293
Qy      1576 GAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1632
Db      1394 GAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1453
Qy      1633 ACCGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1692
Db      1454 GCGGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1513
Qy      1693 GCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1752
Db      1514 GTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Qy      1753 CCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1812

```

```

Db      1571 CCCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1630
Qy      1813 GCGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1872
Db      1631 GCGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
Qy      1873 GCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1932
Db      1691 GCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1750
Qy      1933 TGACTTGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1949
Db      1751 GTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1767

RESULT 7
AAH08620
ID      AAH08620 standard; cDNA; 765 BP.
XX
AC      AAH08620;
XX
DT      26-JUN-2001 (first entry)
XX
DE      Human cDNA clone (5'-primer) SEQ ID NO:5455.
XX
KW      Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS      Homo sapiens.
XX
PN      EP1074617-A2.
XX
PD      07-FEB-2001.
XX
PF      28-JUL-2000; 2000EP-0116126.
XX
PR      29-JUL-1999; 99JP-0248036.
PR      27-AUG-1999; 99JP-0300253.
PR      11-JAN-2000; 2000JP-0118776.
PR      02-MAY-2000; 2000JP-0183767.
PR      09-JUN-2000; 2000JP-0241899.
XX
PA      (HELI-) HELIX RES INST.
XX
PI      Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI      Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR      MPI; 2001-318749/34.
XX
PT      Primer sets for synthesizing polynucleotides, particularly the 5602
PT      full-length cDNAs defined in the specification, and for the detection
PT      and/or diagnosis of the abnormality of the proteins encoded by the
PT      full-length cDNAs -
XX
PS      Claim 1; SEQ ID 5455; 2537bp + CD ROM; English.
XX
XX
XX      The present invention describes primer sets for synthesizing 5602
XX      full-length cDNAs defined in the specification. Where a primer set
XX      comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX      to the complementary strand of a polynucleotide which comprises one of
XX      the 5602 nucleotide sequences defined in the specification, where the
XX      oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX      of an oligonucleotide comprising a sequence complementary to the
XX      complementary strand of a polynucleotide which comprises a 5'-end
XX      sequence and an oligonucleotide comprising a sequence complementary to a
XX      polynucleotide which comprises a 3'-end sequence, where the
XX      oligonucleotide comprises at least 15 nucleotides and the combination of
XX      the 5'-end sequence/3'-end sequence is selected from those defined in
XX      the specification. The primer sets can be used in antisense therapy and
XX      in gene therapy. The primers are useful for synthesizing polynucleotides,
XX      particularly full-length cDNAs. The primers are also useful for the
XX      detection and/or diagnosis of the abnormality of the proteins encoded by
XX      the full-length cDNAs. The primers allow obtaining of the full-length
XX      cDNAs easily without any specialised methods. AAH0166 to AAH1628 and

```



```

Db      233 GGAACAGAGATCTGTCCTGTAAGAGCCAGCCGAGCTGCGGCGCATTTGGGCGCGTTT 174
Qy      2004 GTTAAGCGGACATCTTTGCGGAGCCAGTGGCGTCTCAACACCCCATGACACAGCC 2063
Db      173 GTTAACGGGACATCTTTGCGGAGCCAGTGGCGTCTCAACACCCCATGACACAGCC 114
Qy      2064 ATCTGTGTAACCTCAGAGATCTGTTTCAACCATGTAACACACATATGATGAT 2123
Db      113 ATCTGTGTAACCTCAGAGATCTGTTTCAACCATGTAACACACATATGATGAT 54
Qy      2124 TGTATTAGTGTGTAAGAAACACAGCTCGTAAATAAACAGACGGGTGACCCGC 2176
Db      53 TGTATTAGTGTGTAAGAAACACAGCTCGTAAATAAACAGACGGGTGACCCGC 1

RESULT 9
ABX11430
ID      ABX11430 standard; cDNA, 3744 BP.
XX
AC      ABX11430;
XX
DT      09-MAY-2003 (first entry)
XX
DE      Human caspase recruitment domain containing protein, CARD-11X, cDNA.
XX
XX      CARD, caspase recruitment domain; apoptosis; cell adhesion; inflammation;
XX      cytokine receptor signaling; cancer; glioma; carcinoma; adenocarcinoma;
XX      CARD-containing polypeptide associated disorder; sarcoma; melanoma; ss;
XX      hamartoma; leukemia; lymphoma; keratinocyte hyperplasia; neoplasia;
XX      keloid; benign prostatic hypertrophy; inflammatory hyperplasia; fibrosis;
XX      xeroderma; allergy; arthritis; lupus; Sjogren's syndrome; sepsis; gene;
XX      Crohn's disease; ulcerative colitis; graft versus host disease; stroke;
XX      abnormal cell death disease; myocardial infarction; heart failure; human;
XX      neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV;
XX      CARD-11X; caspase activator; caspase inhibitor.
XX
OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      1..3744
XX      FT      /*tag= a
XX      FT      /product= "CARD-11X"
XX      FT      34..309
XX      FT      /*tag= b
XX      FT      /note= "Encodes caspase recruitment domain (CARD)"
XX      FT      388..1344
XX      FT      /*tag= c
XX      FT      /note= "Encodes Ezrin/radixin/moesin (ERM) domain"
XX      FT      2175..2514
XX      FT      /*tag= d
XX      FT      /note= "Encodes post synaptic density disc-large zo-1
XX      FT      (PDZ) domain"
XX
XX      US2002164703-A1.
XX
XX      07-NOV-2002.
XX
XX      19-DEC-2001; 2001US-0032159.
XX
XX      21-DEC-2000; 2000US-257457P.
XX
XX      (PAWL/) PAWLOWSKI K.
XX      PA      (REED/) REED J C.
XX      PA      (GODZ/) GODZIK A.
XX
XX      Pawlowski K, Reed JC, Godzik A;
XX
XX      WPI; 2003-288137/28.
XX      DR      P-PSDB; ABG76061.
XX
XX      New isolated CARD-containing nucleic acids, useful for the diagnosis
XX      and treatment of disorders with aberrant expression or activity of the

```

```

PT      CARD-containing polypeptide, such as cancer, stroke, arthritis, heart
PT      failure and AIDS
XX
XX      Claim 1; Fig 2; 34pp; English.
XX
XX      The invention relates to an isolated nucleic acid molecule encoding a
XX      caspase recruitment domain (CARD) containing polypeptide. CARD containing
XX      polypeptides are involved in apoptosis (as caspase activators and caspase
XX      inhibitors), cell adhesion, inflammation and cytokine receptor
XX      signaling. The methods and compositions of the present invention are
XX      useful for the diagnosis and treatment of disorders associated with the
XX      aberrant expression or activity of the CARD containing polypeptide such
XX      as cancer, glioma, carcinoma, adenocarcinoma, sarcoma, melanoma, keloid,
XX      hamartoma, leukemia, lymphoma, keratinocyte hyperplasia, neoplasia,
XX      benign prostatic hypertrophy, inflammatory hyperplasia, fibrosis,
XX      xeroderma, allergy, arthritis, inflammatory diseases such as arthritis, lupus,
XX      Sjogren's syndrome, Crohn's disease, ulcerative colitis, graft versus
XX      host disease, sepsis, abnormal cell death diseases such as stroke,
XX      myocardial infarction, heart failure, neurodegenerative diseases like
XX      Parkinson's disease and Alzheimer's disease, and HIV infection. The
XX      present sequence represents cDNA encoding the human caspase recruitment
XX      domain containing protein, CARD-11X.
XX
XX      Sequence 3744 BP; 950 A; 1076 C; 1117 G; 601 T; 0 other;
XX
XX      Query Match      17.3%; Score 375.8; DB 25; Length 3744;
XX      Best Local Similarity 56.9%; Pred. No. 1.7e-56;
XX      Matches 817; Conservative 0; Mismatches 547; Indels 73; Gaps 4;
XX
Qy      157 ACGAGACGATGACGAGTGTGGAACGTCCTGAGGGCTTCCGGGTAGCCTCAGCTCG 216
Db      26 AGGAGGAGAGAGACCCCTTGGAAGATGTGAGTGTAAACCGGACATGCTACCGCGT 85
Qy      217 TCATGACCCCTCAGCATCAACCTTACCTGCGGCAAGTSCAAGTCTCGAACCTTAATG 276
Db      86 ATATCAACCTGCGCAAGCTCAAGCCCTACCTGCTGATGTAAAGTATGATGAGCAGG 145
Qy      277 ATGAGAGAGAGTGTCTAGCGACCCCAACCTGTGTATCTCCGAAACGAAATGGGTGTGC 336
Db      146 ATGAAGATGAAGTGTATTATGCCCCCTATGCTGCATCCAAATCAACGACAGACCGCGC 205
Qy      337 TCCTGGAATCCTGAGCGGACCGGCGCAAGGGGTACGTGCGCTTCCGAGAGCTCG 396
Db      206 TGTGGAATCTTCTACATACCAAGGGGCAAGGGGCTATGTGCTCTTCTTGAGAGCTTAG 265
Qy      397 AGCTCTACTACCGGAGCTGTATCAAGAGTGTACAGGACAGGAGCGGCGCGCTCTTCT 456
Db      266 AATTTTATTACCAAGATGTATCAAACTGTGACTGGAAAGAGCCACTGGAGATCTT 325
Qy      457 CCATATCATGACGCGTCCGGGAGTCAAGGCTGTGACTCACTGCTGATGAGGTCA 516
Db      326 CCACATGTGTGTGAGAGAGGCGCACGAGGCTCACCACACTCTGTATGAGACGAGTCA 385
Qy      517 TGAAGCTGTGAAGAAGAGTGCAG-----GACGTACCGGCGCTGC 555
Db      386 TCAAGCTGTGAAGAAGATGAAGGCGCAAGACCTGTCAACCTGTGAGCTGTGCGAGT 445
Qy      556 TGAGCTCCAAAGATGATCTTCAAGAGCTGCGGGTGAAGAGCAGCTGCTGCGCAAGC 615
Db      446 TCGGAGCTGTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 505
Qy      616 ACCAGAGCGTGTGAGAGAGCTCAAGAGAGAGTGTGAGAGCGCGGAGCGGAGCTCAAGC 675
Db      506 TCCAGAGCGGTACTACAAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 565
Qy      676 GCTGCAAGAGAGAACTACGACTGTGCGCTGCGCTGCGGAGACAGAGTGAAGAGAG 735
Db      566 AGGTGAAGAGAGCACTACCACTTAGCCATGCGCTACGCAAGTCTAGTGAAGAGAG 625
Qy      736 GCGCGCGCTCATGCGGAACGTTGACCTGTGAGAGTGTGACAGCTCAAGCAGAGCC 795
Db      626 ACATGCGGCTCATGAGAGAGCGAGACTTCAACTGTGAGATGATGACTTAAGACCGGT 685

```

```

QY 796 TCATGAAGGCCGAGAGCACTGCGAGGTGAGCGCAAGCAGCTGAACTCAGGCACG 855
DB 686 TGATTAAGATGAGAGAGATGTAAGCTGAGAGAAATAGTCTTAAACTGAAGATG 745
QY 856 CCATGAGAGACGGGCCCAAGCAGAGAGTGTCTGTGGAGCTGCGACAGAGAGAGCCCTGC 915
DB 746 ACATTGAAATCGGCCCAAGAGAGAGAGTGTCTGGAATCGAGCGGGAATGAATATG 805
QY 916 TCACAGGCCCGGGGTGACAGAGCTGAGAGGCTCCGTCAGAGGGGAA-----GCTGG 966
DB 806 TGAAGACAAAACACAGAGCTGCAATCATCATTCAGGCCCGGAGACCGACCTGCGCAG 865
QY 967 ACAGAGACAGCCCTTACATCAGAGTACTGAGAGAGAGTGTGTGCGCAGAGGCTGCGGAC 1026
DB 866 ACTGAGACAGAGCCATCTGAGCATCTTGAACACGACCGCAAGAGAGCCCTGAGAGACA 925
QY 1027 ACCAGAGACAGGCCACCACTTCTCCCTGCGAAGAGACTTCGCGCAGAGGAGGCC 1086
DB 926 GGCAGAGCTGTGTCAACAGGATCTACAACCTGCGAGAGAGGCCCGCCAGAGAGAGC 985
QY 1087 GAGCCTTCGGTGTGATGAGAGAGAGATGTTGAGCTGCGAGTGTCTGCACTACGTA 1146
DB 986 TGCAGACAAAGTACCTGAGAGAGAGAGAGCTGAGAGTCAAGTCTCAACCTGGAA 1045
QY 1147 AGGACTCCANATGTATACAGAGACCGCATCGAGCCATCTGTCAGATGAGAGAGTGC 1206
DB 1046 AGGACTGTAAATGTATACAGAGACCGCATGAAACAGTGTATGTCTGCACTGAGAGAGTGG 1105
QY 1207 CCATTGAGCGGAGACAGAGACACAAATGAGAGGGCTGTGACAGCTCCGCGCCAGCG 1266
DB 1106 AGCGGAGCGGAGACAGAG-----ACA 1127
QY 1267 GCTTGACGTCTCCGAGAGCTCTGTGTGAGTGTGAGGCGCGCGGCGCAGAGGCCAGCA 1326
DB 1128 GCGTGTGGCTTTCAGAGAGACCTGCATCA-----AGTCTCAACACAGAGCGTGCAC 1182
QY 1327 AGCTTGGGGCCCTCACTAGAGGGTGGCGCTGTGTCTGTCCGTCAGGCGCATAGCCAGCG 1386
DB 1183 AGCAAGGGTGGAGCCATGCGCTGTGTATGATGCGCTTAAATGAAGAGGGCTTTCAC 1242
QY 1387 GAGAGCTGACAGCAGACAGAGCCCGGGGCTGACAGAGAGAGAGCGGCTGCGGAAGCAG 1446
DB 1243 GATGAGCTGAGACAGAGTACTCCAGTCTTAATCGAAAGAGACAGATACAGAGAGCAG 1302
QY 1447 GTGCGGAGCTGGGAGAGAGCGGATAGCTGACAGCTGAGAGTTCAGTGTGAGAGCG 1506
DB 1303 ATCCGAGAGCTGGAGAGAGAGACAGAGATGAGATCGAGATGTGCGCGGAGAGGCC 1362
QY 1507 CAGTACTGCGCTGAGAGAGAGGCTCAGAGCGGAGAGAGCTGAGAGCGTGTCTG 1563
DB 1363 TGCATCGTCAACCTGAGAGAGAGAGCTGCGCGCTTTCAGAGAGACAGAACCACTG 1419

RESULT 10
AAS05389
ID AAS05389 standard; cDNA; 4275 BP.
XX AAS05389;
AC
XX 12-SEP-2001 (first entry)
DT
XX
DE Human caspase recruitment domain, CARD-11 cDNA sequence.
XX
XX Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
XX apoptosis; hyperproliferative disorder; autoimmune; neurological;
XX inflammatory disorder; viral infection; stress-related response; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 327..3770
FT /tag= a
FT /product= "CARD-11"

```

```

PT /note= "ORF is specifically claimed"
XX
XX WO200140468-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 01-DEC-2000; 2000WO-US32716.
PF
XX
XX 03-DEC-1999; 99US-0168780.
PR 18-FEB-2000; 2000US-0507533.
PR 25-FEB-2000; 2000US-0513904.
PR 10-OCT-2000; 2000US-0685791.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX Bertin J;
PI
XX WPI; 2001-367809/38.
DR
XX P-PSDB; AAU01207.
DR
XX
XX Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10,
PT CARD-11, useful as targets for therapy, as immunogens, and in screening
PT and detection assays -
XX
XX Claim 2; Fig 14A-14C; 145pp; English.
PS
XX
XX The present sequence encoding for novel human caspase recruitment
XX domain, CARD-11 is isolated from a human T-cell cDNA library.
XX Also described are novel human sequences for CARD-9 and CARD-10
XX (AAU01205, AAU01206) and rat CARD-9 (AAU01204). CARD-9, CARD-10 and
XX CARD-11 interact with Bcl-10 which is thought to activate nuclear factor
XX (NF)-kappaB and apoptosis. The sequences of the invention can be used for
XX treating a disorder associated with abnormal levels of apoptosis by
XX modulating the expression or activity of CARD-9, CARD-10, or CARD-11.
XX They can be used for the treatment of hyperproliferative disorders
XX (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus),
XX neurological disorders (e.g. Alzheimer's disease), inflammatory disorders
XX (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD
XX polypeptide, polynucleotide and an antibody which selectively binds to
XX CARD can be used in screening and detection assays (e.g. chromosomal
XX mapping, tissue typing), predictive medicine (prognostic assays,
XX monitoring clinical trials, and therapy (treatment and prophylaxis). The
XX CARD polypeptide may be used to screen for drugs that bind to and/or
XX modulate it. CARD sequences are potential targets for regulating
XX inflammation, cancer, NF-kappaB signaling, stress-related response and
XX apoptosis in human disease. A host cell containing a polynucleotide
XX encoding CARD can be used to create transgenic animals.
XX
XX Sequence 4275 BP; 1045 A; 1255 C; 1320 G; 655 T; 0 other;
SQ
XX
XX Query Match 17.1%; Score 372.2; DB 22; Length 4275;
XX Best Local Similarity 60.5%; Pred. No. 7.2e-56;
XX Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;
XX
XX 157 ACAGAGACGATGACGAGTGTGAGAGCTCTGAGAGGCTTCCGGGTGAGCTCACTCG 216
DB 352 AGGATGAGAGAGAGCGCTGTGTGGAGATGTGAGTGAACCGGACAGTCTAGCGGCT 411
QY 217 TCATGACCCCTCAGAGCATACACCTTACCTGGGAGTGCAGAGTCTGAAACCTGATG 276
DB 412 ATATCAACCTTGCAGAGCTCAGCCCTTACCTGGTGTGATGATGATGAGACAG 471
QY 277 ATGAGAGAGAGTGTGAGAGAGCCCACTGATCCAGCAAGAGAGAGAGTGGTGTG 336
DB 472 ATGAGAGTGAAGTGTCTTATGCCCCCTTATGCTGCATCAAGATCAACAGAGAGCGCGC 531
QY 337 TCCTGACATCTCGACAGCGAGCCGACAGAGGCTACGTGCTTCTCGAGAGCTGTG 396
DB 532 TGTGAGCATTTACATACCAAGAGGAGAGAGGCTATGTGTCTTCTGAGAGCTGAG 591
QY 397 AGCTTACTACCGCAGCTGTGTACAGAGGTACAGAGAGAGAGAGAGCGCGGCTTCT 456
DB 592 AATTTTATTACCGAGAGTGTACAACTGTGTGCTGGAGAGAGAGCCACTCGAGATCT 651

```

```

QY 457 CCATGATCATCGACGCTCCGGGAGTCAAGCCTGATCTGATGATGATGATCA 516
DB 652 CCACCACTTGTGTGGAGGAGAGGCGACAGGGCTCTCAAGACTTCTGATGAACGAGGTCA 711
QY 517 TGAAGCTGCAAGAAAGGTGCAGGAC-----CTGACCGGCGCTGC 555
DB 712 TCAAGCTGCAGCGCAGATGAAGGCCAAGGACCTGCAACGCTGCGAGCTGCGCCAGGT 771
QY 556 TGAGCTCCAAAGATGATCTTCATCAAGAGAGTGGCGGTGAAGGACAGCTGTGCGCAAGC 615
DB 772 TGGGGAGAGCTGAGAGATGAGAGAGAGAGATGACGCTGACGCGCTGGAGCTCTAACT 831
QY 616 ACCAGAGCGTGTGCAAGGCTCAAGAGAGAGTGCAGAGCGCGGACCGCGAGCTCAAGC 675
DB 832 TCCAGAGCGGCTACTCAAGATGAGAGAGAGAGCGGAGCAGCTCAATGACGAGCTGTCA 891
QY 676 GCTGCAAGAGAGAGAACTACGACCTGGCCCTGGCGGCGACAGAGTGAAGAGAGAG 735
DB 892 AGGTGAAGAGAGAGCACTACCTAGCTAGCGCTAGCGCTAGGAGAGAGAGAG 951
QY 736 GCGCGCGCTCATGCGGAGCCGTGACCTGAGCTGAGATGACCACTCAAGCAGACAGCC 795
DB 952 ACATGCGGTCTATGAGAGAGCGGAGACTCTCACTCGAGTGCATGACTTAAGCAGCGGT 1011
QY 796 TCAATGAAGCGGAGAGAGAGAGTGAAGTGAAGCGCAAGCAGCTGAAGCTCAGGACG 855
DB 1012 TGATTAAGATGAGAGAGAGATGTAAGCTGAGAGAAATCACTCTTAAATCAAGAAATG 1071
QY 856 CCATGAGAGAGCGGCGGAGAGAGAGTCTGTGGAGCTGCGACGAGAGAGAGCGCTGC 915
DB 1072 ACATTAAGAAATCGGCGGAGAGAGAGAGAGTCTGGAATCTGAGAGCGGAGAGATGAATGC 1131
QY 916 TCCAGCGCGGAGTGAAGAGTGAAGAGCTCCGCTCCAGAGAGAGAGAG-----GCTGC 966
DB 1132 TGAAGACCAAAAACAGAGAGTGAAGTCAATCCAGCGCGGAGAGAGAGAGCTGTCAG 1191
QY 967 ACAGAGAGAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1026
DB 1192 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1251
QY 1027 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
DB 1252 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1311
QY 1087 GAGCGCTCCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1146
DB 1312 TGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371
QY 1147 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
DB 1372 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
QY 1207 CCATTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
DB 1432 AGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1448

```

```

RESULT 11
ABA00334
ID ABA00334 standard; cDNA; 4276 BP.
XX
AC ABA00334;
XX
DT 09-DEC-2002 (first entry)
XX
DE Human CARD-11 cDNA.
XX
KW Gene; rat; human; caspase recruitment domain; CARD-9; CARD-10;
KW CARD-11; apoptosis; inflammation; cell growth; cell death;
KW lymphocyte activation; cancer; melanoma; autoimmune disease;
KW arthritis; neurological disorder; Alzheimer's disease; ss.
XX

```

```

OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 328..3771
FT /tag= a
FT /product= "CARD-11"
XX
PN MO200270652-A2.
XX
PD 12-SEP-2002.
XX
PF 28-FEB-2002; 2002WO-US06147.
XX
PR 02-MAR-2001; 2001US-0738412.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Berlin U;
XX
PI WPI; 2002-698749/75.
XX
DR P-PSDB; AAG79555.
XX
XX
PT CARD-9, CARD-10 or CARD-11 polypeptides and polynucleotides, useful for
PT treating disorders associated with inappropriate apoptosis or
PT lymphocyte activation, e.g. cancer
XX
PS Disclosure; Fig 14; 151pp; English.
XX
XX
CC This sequence encodes human caspase recruitment domain (CARD)-11.
CC CARD proteins play roles in apoptotic and inflammatory signaling
CC pathways. CARD-9, -10 and -11 participate in the network of
CC interactions that modulate caspase activity. They are thought to be
CC useful as modulating agents for regulating a variety of cellular
CC processes including cell growth and cell death. CARD proteins and
CC nucleic acids are useful for treating a disorder associated with
CC inappropriate apoptosis or lymphocyte activation or for diagnosing
CC subjects having or that are at risk of developing a disorder associated
CC with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such
CC as cancer e.g. melanoma, autoimmune disorders e.g. arthritis, or
CC neurological disorders e.g. Alzheimer's disease.
XX
SQ Sequence 4276 BP; 1045 A; 1256 C; 1320 G; 655 T; 0 other;
XX
Query Match 17.1%; Score 372.2; DB 24; Length 4276;
Best Local Similarity 60.5%; Pred. No. 7.2e-56;
Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;
QY 157 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
DB 353 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412
QY 217 TCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
DB 413 ATATCAACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 472
QY 277 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 336
DB 473 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
QY 337 TCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
DB 533 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 592
QY 397 AGCTCTACTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 456
DB 593 AATTATTAATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 652
QY 457 CCATGATCATCGACGCTCCGGGAGTCAAGCCTGATCTGATGATGATGATCA 516
DB 653 CCACCACTTGTGTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 712
QY 517 TGAAGCTGCAAGAAAGGTGCAGGAC-----CTGACCGGCGCTGC 555

```

Db	713	TCGAAGCTGCAAGCAGATGAAAGCCCAAGACCTTGCAACGCTGCGAGCTGTGCCAGGT	772
QY	556	TGAGCTCCAAAAGATGACTTCACTCAAGAGCTGCGGGTGAAGACAAGCTGTGCGCAAGC	615
Db	773	TGCGCGCAGCTGAGAGATGAGAAAGACGAAGACGCTGACCCGCGTGGAGCTGTCTAACTT	832
QY	616	ACCAGGACCGGTGTCAGAGGCTCAAGAGGAGTGCAGAGCCCGGCAAGCCGACAGTCAAGC	675
Db	833	TCCAGGAGCCGTTACTCAAGATGAAGAGACGGGACAGCTTCAATGACGAGCTTGCTCA	892
QY	676	GCTTCAAGGAGAGAACTTCCAGCTGGCCATCGCCTTGCCGACACAGAGTGAAGAGAAG	735
Db	893	AGGTGAAGAGACGACACTGACAACTTAAGCATGCGCTACGCAACAGTCACTGAGGAGAAGA	952
QY	736	GCGCCGCGGCTCATGCGGGAACCTGTACTCTGCACTGTGAATTGACAGTCAAGCAAGCC	795
Db	953	ACATGCGCGTTCATGAGGAGCGGAGCCCTCCAACTCGAGATGATCAGCTTAAGGACCGGT	1012
QY	796	TCATGAAGAGGCGGAGACGACTGCAAGGTGGAGGCCAAGCAACAGCTGAAGTCAAGCACAG	855
Db	1013	TGAATTAAAGTGAAGAGAAATGTAAAGCTGGAGAGAAATCAAGTCTTTAAACTGAAAGATTG	1072
QY	856	CCATGAGACAGCGGCCCAAGCAGGAGCTGCTGTGGAGCTTCAGACAGGAGAGGCCCTGC	915
Db	1073	ACATTGAAAAATCGGCCCAAGAGAGACAGAGTTCCTGGAACTGGACGCGGAGAAATGAATTGC	1132
QY	916	TCCAGGCCCGGGTGCAGGAGCTGGAAGCTTCCTCGTCCAGAGGGAAA-----GCTGG	966
Db	1133	TGAAGACCAAAAAACAGAGAGCTGCAGTCCATCTCAGGCGGGGAGCGCAGCCTGGCAG	1192
QY	967	ACAGAGACAGCCCTTACATCCAGGTACTGGAGAGGAAATGCGCGCAGGCGGTTGCGGAACC	1026
Db	1193	ACTGAGACMAAGGCCATCTTGACATCTTTGGAACAAGACCGCAAGAGAGCCCTTGAGAGCA	1252
QY	1027	ACCAGGAGCAGGGCCAAACCATCTTTCTCCCTGCGCAAGAACCTCGCCAGGAGCGAGGCC	1086
Db	1253	GCGAGGAGCTGTGTACAAGGATCTTACAACCTGCAAGAGAGAGGCCCGCCAGGACAGAGAGC	1312
QY	1087	GAGCGCTTCGGTGCATGGAGGAGAGAGATGTTGAGCTGCAAGTCTGCGACTTACGTGA	1146
Db	1313	TGCGAGACAAGTACTTGAGGAGAGAGAGGAGACTGAGACTCAAGTCTCAACCTTGGGAA	1372
QY	1147	AGGACTCCAAAGATGTACAAGAGCCGCAATCGAGGCCATCTGTGTGAGATGGAGAGAGTGC	1206
Db	1373	AGGACTGTGAATGTACAAGACCGCATGAACAACGATCATCTGTCACTGTGAGGAGAGGTGG	1432
QY	1207	CCATTGACGGGAGCCAG 1223	
Db	1433	AGCGGAGCGGAGCCAG 1449	

	RESULT 12
ACCS0413	
ID	ACCS0413 standard; cDNA; 1663 BP.
XX	
AC	ACCS0413;
XX	
DT	12-JUN-2003 (first entry)
XX	
DE	Human secreted protein coding sequence, SEQ ID 80.
XX	
KM	Cardiac; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;
KM	vulnerable; antiinflammatory; neurotropic; neuroprotective;
KM	antiparkinsonian; gene therapy; human; cardiovascular disorder;
KM	gene; ss.
XX	
XX	
OS	Homo sapiens.
XX	
XX	
PN	MO200295010-A2.
XX	
PD	28-NOV-2002.
XX	
PF	19-MAR-2002; 2002MO-US09785.

PR	21-MAR-2001; 2001US-277340P.
FR	19-JUL-2001; 2001US-306171P.
PR	13-NOV-2001; 2001US-331287P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	
XI	Rosen CA, Ruben SM;
XX	
DR	WPI; 2003-129429/12.
XX	
PT	Novel human secreted proteins, useful for detecting, preventing,
PT	diagnosing, prognosticating, treating and/or ameliorating
XX	cardiovascular disorders such as arrhythmia -
PS	
XX	Claim 21; SEQ ID 80; 1881pp; English.
CC	The present invention relates to novel human secreted proteins
CC	(ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The
CC	proteins and their coding sequences are useful for the preparation of a
CC	diagnostic or pharmaceutical composition for diagnosing or treating a
CC	cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
CC	coronary arteriosclerosis and myocardial ischemia), neural disorders,
CC	immune system disorders, muscular disorders, reproductive disorders,
CC	gastrointestinal disorders, pulmonary disorders, renal disorders,'
CC	proliferative disorders and/or cancerous diseases and conditions, for
CC	wound healing and epithelial cell proliferation, to treat inflammation or
CC	infection, for treating thrombosis and arteriosclerosis, for treating or
CC	preventing neural damage which occurs in neuronal disorders or
CC	neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC	disease, to enhance bone and periodontal regeneration and aid in tissue
CC	transplants or bone grafts, to prevent skin aging or hair loss, to
CC	stimulate growth and differentiation of hematopoietic cells and bone
CC	marrow cells when used in combination with other cytokines, to maintain
CC	organs before transplantation or for supporting cell culture of primary
CC	tissues, to increase or decrease differentiation or proliferation of
CC	embryonic stem cells, or to modulate mammalian characteristics or
CC	metabolism.
CC	Note: The sequence data for this patent was published in electronic
CC	format and is available from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 1663 BP; 414 A; 481 C; 512 G; 256 T; 0 other;
Query March	16.9%; Score 367.4; DB 25; Length 1663;
Blast Local Similarity	82.4%; Pred. NO. 4.6e-55;
Matches 467; Conservative	0; Mismatches 26; Indels 74; Gaps 1;

QY	1884	CCCTTTCAGAGCTCTGCACACAGAGACAGAGTTTTCGGAACCCCCATGACGCAAGGCTTAGC	1743
Db	966	CCCTTCAGGGAGAGCCGGCCGAGGCCCTGAGCCTTCCCCCTTCTCCAGAGACGCAAGGCTTAGC	10225
QY	1744	AGCCGGGAGCCGCCCGAGAGAGAGCCGGCCGCTCAAGAGAGTTTTCAGAACTTACCGC	1803
Db	1026	AGCGGGGAGCGCCCGAGAGAGAGCCGGCGCTTCAAGAGAGTTTTCAGAACTTACCGC	1085
QY	1804	AGGAAGCGCGCTCTCAGAGAGATGCAGAAAGATGCGGCGCAGGGGAGAGAGACCGGGAG	1865
Db	1086	AGGAAGCGCGCTCTCAGAGAGATGCAGAAAGATGCGGCGCAGGGGAGAGAGACCGGGAG	1145
QY	1864	AACACACACGGGACAGCAACACCGGACATGAGGGGCTCTTAGCCGCA-----	1910
Db	1146	AACACACACGGGACAGCAACACCGGACATGAGGGGCTCTTAGCCGACAGCGCAGCGCC	1205
QY	1911	-----	1910
Db	1206	CGACCAAGGACCAACCCACCGGCGCGGCTCTTGCCACCCCGGGGGTGCCGACCGCTTGGGG	1265
QY	1911	-GCAGACTTCCCGCAGAGCGCTGCTGACTTGGCTTGAAACGAGAGATCTGTGCTCCCTGAAA	1965
Db	1266	CGCAGACTTCCCGCAGAGCGCTGCTGACTTGGCTTGAAACGAGAGATCTGTGCTCCCTGAAA	1322
QY	1970	GGCCCAACCGGACTGCGCGGCGCATTTGGGGCGCTTTGTTAAGCGGACCTCATTTTCGGAGG	2022

Accession	Sequence	Position
Db	GGCCACGGGACATGCGCGGCGCATTTG9GGGCGTTTGTTAAGCGGCACTCATTTTGGGAGG	1385
Oy	CCATGCGGGTCTCAACCACCCCCATGACAGGCCATCTGTAACTTCAGAGTCGTCT	2089
Db	CCATGCGGGTCTCAACCACCCCCATGACAGGCCATCTGTGTAACTTGAGATCTGTCTT	1445
Oy	GTTCACCATGTAAACACACATATACATGATCATGTATTAGTGTAGAAAACAGCTG	2149
Db	GTTCACCATGTAAACACACATATACATGATCATGTATTAGTGTAGAAAACAGCTG	1505
Oy	CGTAATTAACAGCAGCGGGTACCCGC	2176
Db	CGTAATTAACAGCAGCGGGTACCCGC	1552

RESULT 13
ABZ71230
ID ABZ71230 standard; cDNA; 1663 BP.

DE	Human secreted protein-encoding gene 41 cDNA clone HDS5H3, SEQ ID NO:51.
XX	
KW	Human, secreted protein, digestive disorder, gastrointestinal disorder,
KW	mouth, oesophagus, stomach, small intestine, large intestine, liver,
KW	billary tract, pancreas, cancer, tumour, hyperplastic disorder,
KW	immune disorder, inflammation, infection, wound healing, drug screening,
KW	chromosome identification, chromosome mapping, cytostatic,
KW	anti-inflammatory, immunosuppressive, vulnerrary, gene therapy, gene, ss.

PT New human secreted proteins and nucleic acids, useful for detecting,
PT preventing, diagnosing, prognosticating, treating and/or ameliorating
XX e.g. gastrointestinal diseases and disorders, or cancers -
PS Claim 21, Page 782, 1216pp, English.

[illegible]

cc of the invention may be used for chromosome identification, chromosome
cc mapping, in gene therapy, for identifying individuals from minute
cc biological samples, as hybridisation probes, and as molecular weight
cc makers. The present sequence represents a human secreted protein-
cc encoding cDNA clone of the invention.

Sequence 1663 BP; 414 A; 481 C; 512 G; 256 T; 0 other,

Query Match:	16.9%;	Score 367.4;	DB 25;	Length 1663;
Best Local Similarity:	82.4%;	Pred. No. 4,6e-55;		
Matches 467;	Conservative 0;	Mismatches 26;	Indels 74;	Gaps 1

Db	966	CCCTCAGGGGAGCCGGCCGGAGCCCGAGCCTTCCCTTCTCCAGGACGCGAGGCTGAGC	10255
QY	1744	AGCGGGAGGCGCGCCCGGAGAGAGAGCGGGCGCGCTCAAAAGAGATTTTGAATCTACCG	18030
Db	1026	AGCGGGGAGCGCGCCCGGAGAGAGAGCGGGCGCTCAAAAGAGATTTTGAATCTACCG	10855
QY	1804	AGGAAGCGCGCTCCAGGAAGATGCAGAAAGGAATGGGGCGAGGGGAGAGAGACCGGGAG	18635
Db	1086	AGGAAGCGCGCTCCAGGAAGATGCAGAAAGGAATGGGGCGAGGGGAGAGAGACCGGGAG	11455
QY	1864	AACACCAACGGGCAAGCGACCAACCGAGACTGAGGGCTCTAGCCGCA-----	1910
Db	1146	AACACCAACGGGCAAGCGACCAACCGAGACTGAGGGCTCTAGCCGCAAGGCGCC	1205
QY	1911	-----	1910
Db	1206	CGACCAAGGACACACCCACCGCGCGCTCTCTGCACCAGGGGTGCGACGCGCTGAGG	12655
QY	1911	-GCAACTTCCCCGAGCGCTGCTGACTTTGGCCCTGGAACGAGGAATCTGGGCCCTGAA	1965
Db	1266	CGCAACTTCCCCGAGCGCTGCTGACTTTGGCCCTGGAACGAGGAATCTGGGCCCTGAA	13255
QY	1970	GAGCCAGCGGACTGCGGGGCAATTGGGGCGCTTTGTAAAGCGGACACTATTTGCGAGG	2029
Db	1336	GAGCCAGCGGACTGCGGGGCAATTGGGGCGCTTTGTAAAGCGGACACTATTTGCGAGG	13855
QY	2030	CCATGCGGGTCTCAACACCCCAATGCAACAGCCATCTGTAACTTCAGAGTGTTC	2089
Db	1386	CCATGCGGGTGTCAACACCCCAATGCAACAGCCATCTGTAACTTCAGAGTGTTC	1445
QY	2090	GTTTCACCATGTAAACACAAATCAATGATCATTTATTTAGTTAGAAACACAGCTG	2149
Db	1446	GTTTCACCATGTAAACACAAATCAATGATCATTTATTTAGTTAGAAACACAGCTG	1505
QY	2150	CGTAATTAACAGGACGGGTAACCGGC	2176
Db	1506	CGTAATTAACAGGACGGGTAACCGGC	1532

RESULT 14
AAD05585
ID AAD05585 standard; cDNA; 1687 BP.

DE Human secreted protein-encoding gene 7 CDNA clone HBP5H3, SEQ ID NO:17
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; hematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiotensin disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulnerability;
KW cell culture; chemotaxis; food additive;

XX	binding partner identification; ss.
OS	Homo sapiens.
FX	Key
FH	Location/Qualifiers
FT	153..536
FT	/tag= a
FT	/product= "Human secreted protein"
FT	153..209
FT	/tag= b
FT	mat_peptide
FT	210..533
FT	/tag= c
FT	/product= "Human mature secreted protein"
FN	
PN	WO200134627-A1.
PD	
PD	17-MAY-2001.
PP	
PP	08-NOV-2000; 2000MO-US30628.
PR	
PR	12-NOV-1999; 99US-0164744.
PR	30-JUN-2000; 2000US-0215140.
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Ruben SM, Komatsoulis GA, Baker KP, Young PE,
DR	WPI; 2001-316491/33.
DR	P-PSDB; AAE01776.
PT	New nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
XX	
PS	Claim 1; Page 422-423; 567pp; English.
CC	AAD05579-AA005658 represent cDNAs corresponding to 28 human secreted
CC	protein genes and AAE01770-AAE01849 represent the proteins they encode.
CC	AAE01850-AAE01860 represent human secreted protein fragments or variants.
CC	The genes and their secreted proteins are useful for preventing,
CC	treating or ameliorating medical conditions, e.g., by protein or gene
CC	therapy. Pathological conditions can be diagnosed by determining the
CC	amount of the new protein in a sample or by determining the presence of
CC	mutations in the new genes. Specific uses are described for each of the
CC	28 genes, based on the tissues in which they are most highly expressed,
CC	and include developing products for the diagnosis or treatment of
CC	proliferative disorders, cancer, tumors, foetal and developmental
CC	abnormalities, hematopoietic disorders, diseases of the immune system,
CC	AIDS, autoimmune diseases (e.g., Rheumatoid arthritis), inflammation,
CC	allergies, neurological disorders (e.g., Alzheimer's disease,
CC	Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC	skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC	cardiovascular disorders, angiogenic disorders, kidney disorders,
CC	gastrointestinal disorders, pregnancy-related disorders, endocrine
CC	disorders, and infections. The proteins can also be used to aid wound
CC	healing and epithelial cell proliferation, to prevent skin aging due to
CC	culture, to maintain organs before transplantation, for supporting cell
CC	culture of primary tissues, to regenerate tissues, to identify their
CC	cognate ligands or binding partners, and in chemotaxis, and can be used
CC	as a food additive or preservative to modify storage properties.
CC	Antibodies specific for a protein of the invention can be used in
CC	alleviating symptoms associated with the disorders mentioned above, and
CC	in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC	immunosorbent assay (ELISA). The present sequence represents a human
CC	secreted protein-encoding CDNA of the invention.
XX	
SQ	Sequence 1687 BP; 432 A; 480 C; 514 G; 256 T; 5 other;
Query Match	16.3%; Score 355.4; DB 22; Length 1687;
Best Local Similarity	82.1%; Pred. No. 5.6e-53;
Matches	467; Conservative 0; Mismatches 26; Indels 76; Gaps 2

1684 CCCCTTGAGCCTTCGACACAGAGCGATTTTGGGAAACCCCAGCATGACGAGGCCTGAGC 1743

Db	965	CCCTCAGGGGAGCGCGCGGAGGCCGAGCCTTCCCTTCCAGAGACGACGGCTAGC	1024
Qy	1744	AGCGGGAGCGCCCGAGAGAGAGCGGCGCGCCTCAAAGAGTTTGAAGACTACCGC	1803
Db	1025	AGCGGGAGCGCGCCGAGAGAGAGCGGCGCGCCTCAAAGAGTTTGAAGACTACCGC	1084
Qy	1804	AGGAGAGCGCCCTCAGAGAGATGCAAAAGATAGGCGGACAGGG- GGAAGAGAGCCGGGA	1862
Db	1085	AGGAGAGCGCGCTCAGAGAGATGCAAAAGATAGGCGGACAGGGTGAAGAGAGCCGGGA	1144
Qy	1863	GAAACACCGAGGCGAGCAACCCAGACTGAGAGGCTCCTAGCGCGCA-----	1910
Db	1145	GAAACACCGAGGCGAGCAACCCAGACTGAGAGGCTCCTAGCGCGAGCGGACAGCC	1204
Qy	1911	-----	1910
Db	1205	CCCGACCGAGGACACACCCACCGCGCGCTCTTGCCACCCGGGGGTGCCGACGCTGG	1264
Qy	1911	---GCAAGCTTCCCCGAGCGGTGCTGACTTTGGCTTGAAAGAGAAATCTGGTGCCTGA	1967
Db	1265	GGCCGCAACATTCCTCCGAGCGGTGCTGACTTTGGCTTGAAAGAGAAATCTGGTGCCTGA	1324
Qy	1968	AAGGCCAGCGCGAGCTGCGGGGCAATTGGGGCCGTTGTTAAGCGGCACTCATTTGGCGGA	2027
Db	1325	AAGGCCAGCGCGAGCTGCGGGGCAATTGGGGCCGTTGTTAAGCGGCACTCATTTGGCGGA	1384
Qy	2028	GGCCATGCGGGTGTCTACACACCCCATGACACACGCATCTGTGTAACTTCAGATCTGTT	2087
Db	1385	GGCCATGCGGGTGTCTACACACCCCATGACACACGCATCTGTGTAACTTCAGATCTGTT	1444
Qy	2088	CTGTTTCACCATGTAAACACACATACATGCATGATGATTAGTTTGAAGAAACACAGC	2147
Db	1445	CTGTTTCACCATGTAAACACACATACATGCATGATGATTAGTTTGAAGAAACACAGC	1504
Qy	2148	TGCCTAATTAACAGCACGGGTATCCCGC	2176
Db	1505	TGCCTAATTAACAGCACGGGTATCCCGC	1533
RESULT 15			
ACCS0719			
ID	ACCS0719	standard; cdna; 1687 BP.	
XX	AC		
XX	ACC50719;		
XX			
DT	12-JUN-2003	(first entry)	
XX			
DE	Human secreted protein coding sequence, SEQ ID 386.		
XX			
KW	Cardiac; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;		
KW	vulnerable; antiinflammatory; nootropic; neuroprotective;		
KW	antiparkinsonian; gene therapy; human; cardiovascular disorder;		
KW	gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200295010-A2.		
XX			
PD	28-NOV-2002.		
XX			
PF	19-MAR-2002; 2002WO-US09785.		
XX			
PR	21-MAR-2001; 2001US-277340P.		
PR	19-JUL-2001; 2001US-306171P.		
PR	13-NOV-2001; 2001US-331287P.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Ruben SM;		
XX			
DR	WPI; 2003-129429/12.		
XX			

PT Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating
PT cardiovascular disorders such as arrhythmia -

PS Claim 21; SEQ ID 386; 1881bp; English.

XX
CC The present invention relates to novel human secreted proteins
CC (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The
CC proteins and their coding sequences are useful for the preparation of a
CC diagnostic or pharmaceutical composition for diagnosing or treating a
CC cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
CC coronary arteriosclerosis and myocardial ischaemia), neural disorders,
CC immune system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism.
CC Note: The sequence data for this patent was published in electronic
CC format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 1687 BP; 432 A; 480 C; 514 G; 256 T; 5 other;

Query March 16.3%; Score 355.4; DB 25; Length 1687;

Best Local Similarity 82.1%; Pred. No. 5.6e-53; Mismatches 26; Indels 76; Gaps 2;

Matches 467; Conservative 0; Mismatches 26; Indels 76; Gaps 2;

QY 1684 CCCTTTGACAGCTGACACGAGCAAGTCTTTCGGAACCCCGATGACGAGGCTTGAAC 1743
DB 965 CCTTCAGGGAGAGCGCGCGGAGCCGAGCCTTCCCTTCCAGAGAGGAGGCTGAGC 1024
QY 1744 AGCGGGGAGCGCGCGGAGAGAGCGGCGGCTTCAAGAGATTGAGAACTACCGC 1803
DB 1025 AGCGGGGAGCGCGCGGAGAGAGCGGCGGCTTCAAGAGATTGAGAACTACCGC 1084
QY 1804 AGGAAGCGCGGCTTCAAGAGAGATGCAAGAGATGCGGAGAGG-GAAGAGAGACCGGA 1862
DB 1085 AGGAAGCGCGGCTTCAAGAGAGATGCAAGAGATGCGGAGAGGAGAGAGAGCGGA 1144
QY 1863 GAACACGAGGAG 1910
DB 1145 GAACACGAGGAG 1204
QY 1911 ----- 1910
DB 1205 CCGGACGAGGAGACACCCACCGGCGGCTTCTGACACCGGAGGAGCGCCCTG 1264
QY 1911 ---GAGACTTCCCGAGCGGCTGCTGACTTGGCTGGAACGAGAACTGGTCCCTGA 1967
DB 1265 GCGGCAAGCTTCCCGAGCGGCTGCTGACTTGGCTGGAACGAGAACTGGTCCCTGA 1324
QY 1968 AAGGCGGAGCGGAGCTGCGGAGGAGTTGGGGCGGTTGTAAAGCGGACATTTTGCGGA 2027
DB 1325 AAGGCGGAGCGGAGCTGCGGAGGAGTTGGGGCGGTTGTAAAGCGGACATTTTGCGGA 1384
QY 2028 GGCATGCGGAGTGTCAACACACCCCATGACACGCGCATGTGTAACTTCAGGATCTGT 2087
DB 1385 GGCATGCGGAGTGTCAACACACCCCATGACACGCGCATGTGTAACTTCAGGATCTGT 1444
QY 2088 CTGTTTACCAATGTAACACACATATGATGATGATGATGATGATGATGATGATGATGAT 2147
DB 1445 CTGTTTACCAATGTAACACACATATGATGATGATGATGATGATGATGATGATGATGAT 1504

QY 2148 TCGTAATAAACAAGACAGAGGAGTGAACCGC 2176
DB 1505 TCGTAATAAACAAGACAGAGGAGTGAACCGC 1533

Search completed: February 23, 2004, 10:02:25
Job time : 632 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 09:51:41 ; Search time 4582 seconds

(without alignments)
11542.239 Million cell updates/sec

Title: US-10-032-159A-19

Perfect score: 2176
Sequence: 1 atcaccaggaagtgacacag.....aaacagcaggggtgacccgc 2176

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_hiv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_man.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_pbg.*
27: em_gss_vtl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	933.2	42.9	1104	13	BX358485 BX358485
2	883.6	40.6	940	13	BX329048 BX329048
3	800.8	36.8	819	12	B1524042 B1524042
4	752.8	34.6	775	12	B1907340 B1907340

5	725.4	33.3	765	9	AU142752
6	699	32.1	722	12	B1905841
7	668	30.7	755	13	B1912159
8	650.4	29.9	1091	13	BX358484
9	645.6	29.7	738	12	B1909365
10	636.2	29.2	829	10	BF307389
11	621.4	28.6	1132	12	BM922650
12	587.6	27.0	728	12	B1837662
13	587.4	27.0	728	12	BM470298
14	566.4	26.0	916	13	BX327159
15	550.2	25.3	940	13	BX327150
16	498.8	22.9	757	14	CD366678
17	491.6	22.6	498	12	BM149841
18	483.8	20.9	479	12	BM148244
19	450.2	20.7	455	12	B1821044
20	401.2	18.4	470	14	CB473966
21	399.6	18.4	494	10	BF601607
22	398	18.3	413	9	AU159990
23	379	17.4	677	10	BM474019
24	361.2	16.6	542	14	CD369993
25	341	15.7	673	12	B1524874
26	338	15.5	638	13	B0241925
27	310.6	14.3	691	13	BQ189982
28	299.2	13.7	956	13	BQ646025
29	299	13.7	650	12	BM389471
30	288	13.2	1226	14	CB961156
31	273.6	12.6	281	10	BE242923
32	269.2	12.4	411	10	BF653124
33	264.4	12.2	364	9	A1334650
34	264.4	12.2	388	9	A1307612
35	255.8	11.8	1033	9	AU090784
36	250.2	11.5	400	9	AM079047
37	237.8	10.9	425	14	CB696535
38	237	10.9	261	13	BM100570
39	232.6	10.7	734	9	AJ398341
40	226.8	10.4	721	14	CB499434
41	213.8	9.8	312	10	AM974319
42	208.2	9.6	920	14	CA489572
43	205	9.4	205	9	A1364431
44	193.8	8.9	824	10	BG758149
45	188.2	8.6	460	14	CB325982

ALIGNMENTS

RESULT 1
LOCUS BX358485 1104 bp mRNA linear EST 05-MAY-2003
DEFINITION BX358485 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSOD1039YL23 5-PRIME, mRNA sequence.
ACCESSION BX358485
VERSION BX358485.1 GI:30378239
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1104) J. J. J. and Polayes, D.
AUTHORS Li, W.B., Gruber, C., J. J. J. and Polayes, D.
TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5080.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1039C120P1c1cluster=5080.r. Contact :
Feng Liang Email: fliang@lifeitech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

FEATURES Faraday Avenue Genoscope sequence ID : CS001039CF120P1.
Location/Qualifiers

source 1..1104
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001039Y123"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 239 a 334 c 363 g 165 t 3 others

Query Match 42.9%; Score 933.2; DB 13; Length 1104;
Best Local Similarity 98.4%; Pred. No. 1.5e-164;
Matches 1023; Conservative 3; Mismatches 6; Indels 8; Gaps 8;

```

QY 17 CAGGCGTCCGCGCTGCTCTCCCTCCCTCCAGCCCGGCGAGCATCTCCAGAGGCTCG 76
DB 57 CCGGAGATCCGCGCTGCTCTCCCTCCCTCCAGCCCGGCGAGCATCTCCAGAGGCTCG 116
QY 77 CCGGCGGAGCTCTGCTGCTGCTGAGTGAAGTGGCTCTGGAAGACCTTCAAGCTGCG 136
DB 117 CCGGCGGAGCTCTGCTGCTGCTGAGTGAAGTGGCTCTGGAAGACCTTCAAGCTGCG 176
QY 137 TCGTGAAGCCATTCGAGACTACGAGAACGATGACGAGTGTGGAAGTCTTGAAGGCTT 196
DB 177 TCGTGAAGCCATTCGAGACTACGAGAACGATGACGAGTGTGGAAGTCTTGAAGGCTT 236
QY 197 CCGGCGGAGCTCTGCTGCTGCTGAGTGAAGTGGCTCTGGAAGACCTTCAAGCTGCG 256
DB 237 CCGGCGGAGCTCTGCTGCTGCTGAGTGAAGTGGCTCTGGAAGACCTTCAAGCTGCG 296
QY 257 CAGGCTCTGAGACCTGATGATGAGAGAGAGTGTCTCAAGGACCCCACTGCTCAAGCG 316
DB 297 CAGGCTCTGAGACCTGATGATGAGAGAGAGTGTCTCAAGGACCCCACTGCTCAAGCG 356
QY 317 CAAACGGAAGTGGTGTGCTCTGAGCATCTGACGCGGACCGGACAGGGGCTAAGT 376
DB 357 CAAACGGAAGTGGTGTGCTCTGAGCATCTGACGCGGACCGGACAGGGGCTAAGT 416
QY 377 GCGCTTCTGAGAGAGCTGAGAGCTCTAATCCCGAGCTTAACAAGAGTCAACAGCA 436
DB 417 GCGCTTCTGAGAGAGCTGAGAGCTCTAATCCCGAGCTTAACAAGAGTCAACAGCA 476
QY 437 GGAAGCGGCGCGGCTCTCTCATGATCATGACGCGTCCGGGAGTCAAGGCTGAAGTCA 496
DB 477 GGAAGCGGCGCGGCTCTCTCATGATCATGACGCGTCCGGGAGTCAAGGCTGAAGTCA 536
QY 497 GCTGCTGATGATGAGTCAAGAGTCAAGAGAGTGTCTCAAGGACCCCACTGCTCAAG 556
DB 537 GCTGCTGATGATGAGTCAAGAGTCAAGAGAGTGTCTCAAGGACCCCACTGCTCAAG 596
QY 557 GAGCTCCAAAGATGATTCATCAAGAGAGTGTGGGTGAAGAGACCTGCTGCGCAAG 616
DB 597 GAGCTCCAAAGATGATTCATCAAGAGAGTGTGGGTGAAGAGACCTGCTGCGCAAG 655
QY 617 CCAGAGAGCTGTGAGAGAGTCAAGAGAGTGTGGGAGCGGCGGAGCTCAAGCG 676
DB 656 CCAGAGAGCTGTGAGAGAGTCAAGAGAGTGTGGGAGCGGCGGAGCTCAAGCG 715
QY 677 CTGAGAGAGAGAGACTACGAGCTGAGCATGCGCTGCGGACCAAGAGTGAAGAGAG 736
DB 716 CTGAGAGAGAGAGACTACGAGCTGAGCATGCGCTGCGGACCAAGAGTGAAGAGAG 775
QY 737 CGCGCGCTCATGCGGAGACCTGACCTGACCTGAGATTTGACCAAGTCAAGCAAGCTT 796
DB 776 CGCGCGCTCATGCGGAGACCTGACCTGACCTGAGATTTGACCAAGTCAAGCAAGCTT 835
QY 797 CATGAAGCCGAGAGACGATGGAAGGTGAGCGGCAAGACACGCTGAAGCTCAAGCAAG 856

```

```

DB 836 CATGAAGCCGAGAGACGATGCAAGGTGAGCGGCAAGACACCTGAAGCTCAAGCAAG 895
QY 857 CATGAAGCCGAGAGACGATGCAAGGTGAGCGGAGCTGCTGAGAGCTGACAGAGAGAGCTTGC 915
DB 896 CATGAAGCCGAGAGACGATGCAAGGTGAGCGGAGCTGCTGAGAGCTGACAGAGAGAGAGCTTGC 955
QY 916 TCCAGAGCCCGGAGTGCAGAGAGCTGAGAGAGCTTCCGACAGAGAGAGAGAGAGAGAGCA 975
DB 956 TCCAGAGCCCGGAGTGCAGAGAGCTGAGAGAGCTTCCGACAGAGAGAGAGAGAGAGAGCA 1014
QY 976 GCGCTTCAATCAAGAGTACTGAGAGAGAGTGGCGGAGAGAGCTGAGAGAGAGAGAGAGAG 1035
DB 1015 GCGCTTCAATCAAGAGTACTGAGAGAGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1070
QY 1036 AGGCGCAACACCATCTTCTCC 1055
DB 1071 AGGCGCAACACCATCTTCTCC 1089

```

RESULT 2
BX329048/c 940 bp mRNA linear EST 01-MAY-2003
LOCUS BX329048 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS001039Y123 3-PRIME, mRNA sequence.
ACCESSION BX329048
VERSION BX329048.1 GI:30309837
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 940)
Li W.B., Gruber C., Jesssee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5080.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BA1021ZG08_CS01983_1&cluster=5080.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BA1021ZG08_CS01983_1.

FEATURES
source 1..940
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001039Y123"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 129 a 320 c 271 g 215 t 5 others

ORIGIN

Query Match 40.6%; Score 883.6; DB 13; Length 940;
Best Local Similarity 98.4%; Pred. No. 2.8e-155;
Matches 900; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

```

QY 290 GCTGAGGAGCCCAACCTGATCCGCAAGAGAGAGTGTGCTTCTGAGATCCT 349
DB 940 GTTCAGGAGCCCAACCTGATCCGCAAGAGAGAGTGTGCTTCTGAGATCCT 881
QY 350 GGAGGAGCCGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 409

```

```

Db      880 GCANCGAGCGNCCAGAGGGCTACGT -GCCTTCTCGAGAGCGCTGAGCTGCTACTANCC 822
Qy      410 GCAGCTGTACAGAGAGGTCA CAGGCAAGAGCGCCCGCTTTCTTCATGATCATCA 469
Db      821 GCAGCTGTACAGAGAGGTCA CAGGCAAGAGCGCCCGCTTTCTTCATGATCATCA 762
Qy      470 CGGCTCCGGGAGATTCAGGCTCTGACTGACTGCTGATGAGTCTGAGTCTGATGAGTCTGAGT 529
Db      761 CGGCTCCGGGAGATTCAGGCTCTGACTGACTGCTGATGAGTCTGATGAGTCTGAGTCTGAGT 702
Qy      530 GAAGGTGACAGAGCTGACCGCGCTGCTGAGCTCCAAAGATGATCTTCATCAAGAGTCTGCG 589
Db      701 GAAGGTGACAGAGCTGACCGCGCTGCTGAGCTCCAAAGATGATCTTCATCAAGAGTCTGCG 642
Qy      590 GGTGAAGAGACAGCTGTGCTGCGCAAGCA CAGAGCGCTGTGTCAGAGGCTCAAGAGAGAGTG 649
Db      641 GGTGAAGAGACAGCTGTGCTGCGCAAGCA CAGAGCGCTGTGTCAGAGGCTCAAGAGAGAGTG 582
Qy      650 CGAGGCGCGGAGCGCGGAGCTCAAGCGCTGCAAGAGAGAGAGTCTGAGTCTGCGCTGCG 709
Db      581 CGAGGCGCGGAGCGCGGAGCTCAAGCGCTGCAAGAGAGAGAGTCTGAGTCTGCGCTGCG 522
Qy      710 CTTGCGCCACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
Db      521 CTTGCGCCACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
Qy      770 GAGATTTGACAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 829
Db      461 GAGATTTGACAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 402
Qy      830 CAAGCAACAGCTGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 889
Db      401 CAAGCAACAGCTGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 342
Qy      890 GAGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 949
Db      341 GAGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 282
Qy      950 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1009
Db      281 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
Qy      1010 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1069
Db      221 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 162
Qy      1070 CCGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1129
Db      161 CCGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 102
Qy      1130 GTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1189
Db      101 GTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 42
Qy      1190 GCAGATGAGAGAGAGT 1204
Db      41 GCAGATGAGAGAGAGT 27

```

```

RESULT 3
BIS24042 819 bp mRNA linear EST 29-AUG-2001
LOCUS 603052217F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201572 5'
DEFINITION mRNA sequence.
ACCESSION BIS24042
VERSION BIS24042.1 GI:15348834
KEYWORDS EST.
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/

```

TITLE JOURNAL COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strusberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11505 row: b column: 05
High quality sequence stop: 786.
Location/Qualifiers

FEATURES source

1. 819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5201572"
/lab_host="DH10B"
/clone_1lb="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lungs, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH MGC Library."

BASE COUNT ORIGIN

Query Match 36.8%; Score 800.8; DB 12; Length 819;
Best Local Similarity 99.1%; Pred. No. 8.3e-140;
Matches 805; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

Qy      3 CATCAGGAAGTGCACAGAGGAGTCCGGGAGTCTCTCCCTCCGAGAGCCCGGAGAGATC 62
Db      8 CATCAGGAAGTGCACAGAGGAGTCCGGGAGTCTCTCTCTCTGACAGCCCGGAGAGATC 67
Qy      63 TCCCAAGAGGCTCCGGGAGCCAGAGCTCTGCTGTGTCTGTGCAAGTGTGAGTCTCTGAA 122
Db      68 TCCCAAGAGGCTCCGGGAGCCAGAGCTCTGCTGTGTGTGTGAGTGTGAGTGTGAGAG 127
Qy      123 ACCCTTAGGCTCTGCTGAGGAGCATGTGAGCATAGAGAGATGAGAGTGTGAGAAC 182
Db      128 ACCCTTAGGCTCTGCTGAGGAGCATGTGAGCATAGAGAGATGAGAGTGTGAGAGC 187
Qy      183 GTCTTGAAGAGGCTTCCGGGTGACGCTCACTGGTTCATGAGAGAGAGAGAGAGAGAG 242
Db      188 GTCTTGAAGAGGCTTCCGGGTGAGGCTCACTGGTTCATGAGAGAGAGAGAGAGAGAG 247
Qy      243 TAACCTGCGGAGTGAAGAGTCTGAACCTGATGATGAGAGAGAGAGAGAGAGAGAGAG 302
Db      248 TAACCTGCGGAGTGAAGAGTCTGAACCTGATGATGAGAGAGAGAGAGAGAGAGAGAG 307
Qy      303 AACCTGATCATCCGAAACGAAAGTGGTGTGCTCTGAGATCTGTGAGAGAGAGAGAGAG 362
Db      308 AACCTGATCATCCGAAACGAAAGTGGTGTGCTCTGAGATCTGTGAGAGAGAGAGAGAG 367
Qy      363 CACAAGGAGTACAGAGGCTTCTTCAGAGAGCTGAGAGTCTACTACCCGAGAGTGTACAG 422
Db      368 CACAAGGAGTACAGAGGCTTCTTCAGAGAGCTGAGAGTCTACTACCCGAGAGTGTACAG 427
Qy      423 AAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
Db      428 AAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
Qy      483 TAGAGGCTGACTCAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 542
Db      488 TAGAGGCTGACTCAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 547

```

QY 543 CTGACCGCGCTGCTGAGTCTCAAAATGATTCATCAAGAGCTGCGGTGAAGACAGC 602
 DB 548 CTGACCGCGCTGCTGAGTCTCAAAATGATTCATCAAGAGCTGCGGTGAAGACAGC 607
 QY 603 CTGCTCGGAGAGACAGAGAGCGTGTGCAAGAGCTCAAGAGAGTGCAGAGCGCGAGC 662
 DB 608 CTGCTCGGAGAGACAGAGAGCGTGTGCAAGAGCTCAAGAGAGTGCAGAGCGCGAGC 667
 QY 663 CGGAGCTCAAGCGCTGCAAGAGAGAACTACGACTGCGCTGCGCTGCGACACAG 722
 DB 668 CGGAGCTCAAGCGCTGCAAGAGAGAACTACGACTGCGCTGCGCTGCGACACAG 727
 QY 723 AGTAGAGAGAGAGCGCGCTCATGCGGACCGTGAAGCTGAGATTGACAG 782
 DB 728 AGTAGAGAGAGAGCGCGCTCATGCGGACCGTGAAGCTGAGATTGACAG 787
 QY 783 CTGACGACAGCTCATGAAGCGCGAGACGA 814
 DB 788 CTGACGACAGCTCATGAAGCGCGAGACGA 819

RESULT 4
 BI907340 775 bp mRNA linear EST 16-OCT-2001
 LOCUS 603063637F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212881 5',
 DEFINITION mRNA sequence.

ACCESSION BI907340
 VERSION BI907340.1 GI:16170158
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLM1534 row: 1 column: 10
 High quality sequence stop: 772.
 Location/Qualifiers

FEATURES
 source
 1. 775

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5212881"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."
 BASE COUNT 161 a 238 c 252 g 124 t
 ORIGIN

Query Match 34.6%; Score 752.8; DB 12; Length 775;
 Best Local Similarity 99.0%; Pred. No. 7.8e-11;
 Matches 768; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 4 ATCAGAGAGTGCACAGAGGCTCCGGCGCTGCTCCCTCCCTGAGAGCCCGGAGACACT 63
 DB 1 ATCAGAGAGTGCACAGAGGCTCCGGCGCTGCTCCCTCCCTGAGAGCCCGGAGACACT 60
 QY 64 CCCAGAGGCTCCGGCGCCAGAGCTCTGATGTCTGACAGTGCAGTGGCTCTGAGAGA 123
 DB 61 CCCAGAGGCTCCGGCGG-CAGAGCTCTGATGTCTGACAGTGCAGTGGCTCTGAGAGA 119
 QY 124 CCTCAGGCTGCTGCTGAGAGCCATGTGCACTACGAGAACGATGACAGTGTGGAACG 183
 DB 120 CCTCAGGCTGCTGCTGAGAGCCATGTGCACTACGAGAACGATGACAGTGTGGAACG 179
 QY 184 TCTGAGAGGCTTCCGGGTGACGCTCACCTGGTTCATGACCCCTCACGATGACACTT 243
 DB 180 TCTGAGAGGCTTCCGGGTGACGCTCACCTGGTTCATGACCCCTCACGATGACACTT 239
 QY 244 ACTGCGGCAATGCAAGGTCTCTGAACCTGATGATGAGAGCAGGTGCTGAGACCCCA 303
 DB 240 ACTGCGGCAATGCAAGGTCTCTGAACCTGATGATGAGAGCAGGTGCTGAGACCCCA 299
 QY 304 ACTGCTCATGCGGCAAGCAAGGTGCTCTGACATCTCTGACGCGACCGGCC 363
 DB 300 ACTGCTCATGCGGCAAGCAAGGTGCTCTGACATCTCTGACGCGACCGGCC 359
 QY 364 ACAAGGCTACGTGACCTTCTCTGAGAGCTGAGCTTACTACCGCAGCTGTACAGA 423
 DB 360 ACAAGGCTACGTGACCTTCTCTGAGAGCTGAGCTTACTACCGCAGCTGTACAGA 419
 QY 424 AGGTACACGAGCAAGAGAGCGCGCGCTTCTCTCATGATATGAGAGCGTCCGGAGT 483
 DB 420 AGGTACACGAGCAAGAGAGCGCGCGCTTCTCTCATGATATGAGAGCGTCCGGAGT 479
 QY 484 CAGGCTCATCATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
 DB 480 CAGGCTCATCATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
 QY 544 TGACCGGCTGCTGAGCTCCAAAGATGACTTCATCAAGAGCTCGGGTGAAGACAGCC 603
 DB 540 TGACCGGCTGCTGAGCTCCAAAGATGACTTCATCAAGAGCTCGGGTGAAGACAGCC 599
 QY 604 TGCTGCGAGACACAGAGAGCGGTGTGACAGAGCTCAAGAGAGTGCAGAGCGGACCC 663
 DB 600 TGCTGCGAGACACAGAGAGCGGTGTGACAGAGCTCAAGAGAGTGCAGAGCGGACCC 659
 QY 664 GCGAGCTCAAGGCTGCGAGAGAGAACTACGACTGCGCTGCGCTGCGACACAGA 723
 DB 660 GCGAGCTCAAGGCTGCGAGAGAGAACTACGACTGCGCTGCGCTGCGACACAGA 719
 QY 724 GTGAGAGAGAGAGAGCGCGCGCTCATGCGGAACTGACCTGAGTGAATTGAC 779
 DB 720 GTGAGAGAGAGAGAGCGCGCGCTCATGCGGAACTGACCTGAGTGAATTGAC 775

RESULT 5
 AUI42752 765 bp mRNA linear EST 05-AUG-2002
 LOCUS AUI42752 Y79AA1 Homo sapiens cDNA clone Y79AA100827 5', mRNA
 DEFINITION sequence.
 ACCESSION AUI42752
 VERSION AUI42752.1 GI:11004273
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 765)
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Salto,K., Kawai,Y.,
 Yamamoto,D., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isogai,T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished
 COMMENT Contact: Takao Isogai

Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

source

1..765

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="Y79A1000827"

/cell_type="retinoblastoma"

/cell_line="Y79"

/clone_idb="Y79A1"

/note="Vector: pME18SFL3"

/note="236 c 242 g 123 t 4 others"

BASE COUNT

160 a 236 c 242 g 123 t 4 others

ORIGIN

Query Match 33.3%; Score 725.4; DB 9; Length 765;
 Best Local Similarity 99.0%; Pred. No. 1e-125;
 Matches 759; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

1 ATCATCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCCCGGAGCA 60
 1 ATCATCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCCCGGAGCA 60
 61 TCTCCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCGTGGCTCTG 120
 61 TCTCCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCGTGGCTCTG 120
 121 AGACCTCAGCGTCCGCTGCTGAGGCGTCCGCGCTCCTCCCTCCCTGAGCGTGG 180
 121 AGACCTCAGCGTCCGCTGCTGAGGCGTCCGCGCTCCTCCCTCCCTGAGCGTGG 180
 181 ACCTCCTGAGAGGCTCCGCGCTCCTGAGGCGTCCGCGCTCCTCCCTCCCTGAG 240
 181 ACCTCCTGAGAGGCTCCGCGCTCCTGAGGCGTCCGCGCTCCTCCCTCCCTGAG 240
 241 CTTACCTGAGAGGCTCCGCGCTCCTGAGGCGTCCGCGCTCCTCCCTCCCTGAG 300
 241 CTTACCTGAGAGGCTCCGCGCTCCTGAGGCGTCCGCGCTCCTCCCTCCCTGAG 300
 301 CCAACCTGAGTCCGCGCTCCTGAGGCGTCCGCGCTCCTCCCTCCCTGAGCGG 360
 301 CCAACCTGAGTCCGCGCTCCTGAGGCGTCCGCGCTCCTCCCTCCCTGAGCGG 360
 361 GCCACAGAGGCTCAGTGGCTTCTCCGAGGCTCCGAGGCTCCGAGGCTCCGAG 420
 361 GCCACAGAGGCTCAGTGGCTTCTCCGAGGCTCCGAGGCTCCGAGGCTCCGAG 420
 421 AGAAGTTCACAGGAGAGGAGCGCGCTTCTCCGAGGCTCCGAGGCTCCGAGG 480
 421 AGAAGTTCACAGGAGAGGAGCGCGCTTCTCCGAGGCTCCGAGGCTCCGAGG 480
 481 AGTACGCTGACCTGACCTGCTGATGAGTCAATGAAGCTGAGAGAGAGTGA 540
 481 AGTACGCTGACCTGACCTGCTGATGAGTCAATGAAGCTGAGAGAGAGTGA 540
 541 ACCTGACCGGCTGAGTCCAAAGATGATTCATCAAGAGAGTGGGCTGAAGCA 600
 541 ACCTGACCGGCTGAGTCCAAAGATGATTCATCAAGAGAGTGGGCTGAAGCA 600
 601 GCTGCTGCGAGACCAAGAGAGTGGTGAAGAGTCCCAAGAGAGAGTGGAGG 660
 601 GCTGCTGCGAGACCAAGAGAGTGGTGAAGAGTCCCAAGAGAGAGTGGAGG 660
 661 GCCGCGAGCTCAAGCGCTGAGAGAGAGTGAAGTCAAGAGTGGGCTGGCGG 720

DB 661 GCCGCGAGCTCAAGCGCTGAGAGAGAGTGAAGTCAAGAGTGGGCTGGCGG 718
 QY 721 AGATGAG 766
 DB 719 AATGAG 765

RESULT 6

LOCUS

B1905841 722 bp mRNA linear EST 16-OCT-2001

603062919P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212037 5',

DEFINITION

mRNA sequence.

B1905841

B1905841.1 GI:16168432

EST.

SOURCE

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 722)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL ac:

http://image.llnl.gov

Plate: L14M1532 row: f column: 06

High quality sequence stop: 714.

Location/Qualifiers

1..722

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5212037"

/tissue_type="leukocyte"

/lab_host="DH10B"

/clone_idb="NIH_MGC_118"

/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV

(destroyed); RNA source leukocytes from anonymous pool of

non-activated adult donors. Library is oligo-dT primed

and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

1.2-3.3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 027. Note:

this is a NIH_MGC Library."

BASE COUNT

156 a 216 c 233 g 117 t

ORIGIN

Query Match 32.1%; Score 689; DB 12; Length 722;
 Best Local Similarity 99.7%; Pred. No. 8.9e-121;
 Matches 721; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

80 CCCAGGCTCTGGTGTGTCTGAGTGCAG-GTGGCTCTCTGAGAGACCTTCAGCTG 138
 1 CCCAGGCTCTGGTGTGTCTGAGTGCAGTGTGGCTCTCTGAGAGACCTTCAGCTG 60
 139 CTGAGGCAATGTGGAAGTCAAGAAAGATGAGAGTGTGGAAGCTCTGAGG 198
 61 CTGAGGCAATGTGGAAGTCAAGAAAGATGAGAGTGTGGAAGCTCTGAGG 120
 199 GGGTGAAGTCAAGTGTGGAAGTCAAGAAAGATGAGAGTGTGGAAGCTCTGAGG 258
 121 GGGTGAAGTCAAGTGTGGAAGTCAAGAAAGATGAGAGTGTGGAAGCTCTGAGG 180
 259 AGGTCTGGAAGCTGATGATGAGAGAGTGTGGAAGTGTGGAAGCTCTGAGG 318

```

Db      181 AGGTCCTGAACCTGTGATGAGAGAGAGTGTCTCAGCCAGCCCACTGTCATCCGA 240
Qy      319 AACGGAAGTGGTGTGCTCTCTGACATCTTGACGCGACCCGCAAGAGCTACGTGG 378
Db      241 AACGGAAGTGGTGTGCTCTCTGACATCTTGACGCGACCCGCAAGAGCTACGTGG 300
Qy      379 CCTTCTCGAGACCTTGAGAGCTTCTAATACCCGAGCTGTATACAGAGGTCAAGAGGAAAG 438
Db      301 CCTTCTCGAGACCTTGAGAGCTTCTAATACCCGAGCTGTATACAGAGGTCAAGAGGAAAG 360
Qy      439 AGCGGAGCCGCGCTTCTCTCATATCATGACGCGTCCGAGGAGTCAAGGCTTACTCAGC 498
Db      361 AGCGGAGCCGCGCTTCTCTCATATCATGACGCGTCCGAGGAGTCAAGGCTTACTCAGC 420
Qy      499 TGCTGATGACTGAGTCTGATGAGCTGAGAGAGTGCAGAGCTGACCGCTGCTGTA 558
Db      421 TGCTGATGACTGAGTCTGATGAGCTGAGAGAGTGCAGAGCTGACCGCTGCTGTA 480
Qy      559 GCTTCAAAAGTACTTATCAAGAGCTGCGGTTGAAGACAGCTGCTGCGCAAGCACC 618
Db      481 GCTTCAAAAGTACTTATCAAGAGCTGCGGTTGAAGACAGCTGCTGCGCAAGCACC 540
Qy      619 AGAGAGCTGTGAGAGGCTCAAGAGAGTGCAGAGCTCCGCAAGCTCAAGCGCT 678
Db      541 AGAGAGCTGTGAGAGGCTCAAGAGAGTGCAGAGCTCCGCAAGCTCAAGCGCT 600
Qy      679 GCAAGAGAGAGAACTAGACCTGGCCATGCGCTGGGCAACAGAGTGAAGAGAGAGGCG 738
Db      601 GCAAGAGAGAGAACTAGACCTGGCCATGCGCTGGGCAACAGAGTGAAGAGAGAGGCG 660
Qy      739 CCGGCTCATGCGGACCGTGAAGCTGAGATGACAGCTCAAGCTCAAGCTCAAGCTCA 798
Db      661 CCGGCTCATGCGGACCGTGAAGCTGAGATGACAGCTCAAGCTCAAGCTCAAGCTCA 719
Qy      799 TGA 801
Db      720 TGA 722

RESULT 7
LOCUS      BI912159
DEFINITION 603065408F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214576 5',
            mRNA sequence.
ACCESSION  BI912159
VERSION    BI912159.1 GI:16176140
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 755)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL).
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LHAM1538 row: P column: 01
            High quality sequence stop: 689.
            Location/Qualifiers
                1..755
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5214576"
                /tissue_type="leukocyte"
FEATURES
    source

```

```

/lab host="DH10B"
/clone.lib="NIH_MGC_118"
/note="Vector: pCMV-Sport6, Site 1: NotI, Site 2: EcoRV
(deleted); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is oligo-dT primed
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH MGC Library."
BASE COUNT  157 a 231 c 246 g 121 t
ORIGIN
Query Match      30.7%; Score 668; DB 12; Length 755;
Best Local Similarity 97.3%; Pred.No. 5,7e-115;
Matches 732; Conservative 0; Mismatches 15; Indels 5; Gaps 5;

52  CCGGAGCATCTCCAGAGGCTCCGCGCCAGAGCTCTGTGTGTCTGCAAGTGAAGTGTG 111
Db  5  CCGGAGCATCTCCAGAGGCTCCGCGCG-CCAGCTCTGTGTGTCTGCAAGTGAAGTGTG 63
Qy  112 GCTCTGAGAG-ACCCTGAGCTGCTGAGGCAATGTGAGACTAGAGAAAGATGAC 170
Db  64  GCTCTGAGAGAACTTCAAGCTGCTGCTGAGGCAATGTGAGACTAGAGAAAGATGAC 123
Qy  171 GAGTCTGAAAGCTCTGAGAGGCTTCCGAGTGAAGCTCACTGCTGATGACCCCTCA 230
Db  124 GAGTCTGAAAGCTCTGAGAGGCTTCCGAGTGAAGCTCACTGCTGATGACCCCTCA 183
Qy  231 CGCATCAACCTTACCTGCGAGTGAAGTCTGAACTTATGATGAGAGAGAGTGTG 290
Db  184 CGCATCAACCTTACCTGCGAGTGAAGTCTGAACTTATGATGAGAGAGAGTGTG 243
Qy  291 CTCAGCAGCCCACTGCTGATCCGCAAGAGAGAGTGTGCTCTGCAATCTGTG 350
Db  244 CTCAGCAGCCCACTGCTGATCCGCAAGAGAGAGTGTGCTCTGCAATCTGTG 303
Qy  351 CAGCGAGCCGCAACAAGGCTGAGTGGCTTCTCGAGAGCTGAGCTCACTACCCG 410
Db  304 CAGCGAGCCGCAACAAGGCTGAGTGGCTTCTCGAGAGCTGAGCTCACTACCCG 363
Qy  411 CAGCTGTCAAGAAGTCAACAGGAGCGCCGCTGCTTCTCATGATCACTGAC 470
Db  364 CAGCTGTCAAGAAGTCAACAGGAGCGCG-CCCGCTTCTCATGATCACTGAC 422
Qy  471 GCGTCGAGAGTCAAGCTGATCACTGATGATGATGATGATGATGATGATGATGATG 530
Db  423 GCGTCGAGAGTCAAGCTGATCACTGATGATGATGATGATGATGATGATGATGATG 482
Qy  531 AAGGTGCAAGAGTCAACGCGCTGCTGAGTCCAAAGTATGATGATGATGATGATG 590
Db  483 AAGGTGCAAGAGTCAACGCGCTGCTGAGTCCAAAGTATGATGATGATGATGATG 542
Qy  591 GTGAAGAGCAGCTGCTGCGCAAGCAGAGGCTGAGAGGCTCAAGAGAGAGTGC 650
Db  543 GTGAAGAGCAGCTGCTGCGCAAGCAGAGGCTGAGAGGCTCAAGAGAGAGTGC 602
Qy  651 GAGCGCGAGCGCGAGCTCAAGGCTGCAAGAGAGAACTAGAGCTGCGCTGCGC 710
Db  603 GAGCGCGCGAGCGCGAGCTCAAGGCTG-AGAGAGAGAACTAGAGCTGCGCTGCGC 661
Qy  711 CTGGCGCACCAAGTGAAGAGAGGCGCGCTCATGCGAAGCTGCACTGCACTG 770
Db  662 CTGGCGCACCAAGTGAAGAGAGGCGCGCTCATGCGGAGAGCTGCACTGCACTG 721
Qy  771 GAG-ATTGACAGCTCAAGCAGAGCTCATGA 801
Db  722 GAGCATTGACAGCTCAAGCAGCTGCTGCTGTA 753

RESULT 8
BX38484/c

```


LOCUS	EX358484	1091 bp	mRNA	linear	EST 05-MAY-2003
DEFINITION	EX358484 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI039YL23 3-PRIME, mRNA sequence.				
ACCESSION	EX358484				
VERSION	EX358484.1	GI:30376237			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Enkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.				
TITLE	Full-length CDNA libraries and normalization				
JOURNAL	Unpublished				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5080.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODI039C12NP1&cluster=5080.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI039CF12NP1. Location/Qualifiers				
FEATURES	1..1091				
source	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODI039YL23" /issue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."				
BASE COUNT	153 a 356 c 322 g 237 t 23 others				
ORIGIN					
Query Match	29.9% Score 650.4; DB 13; Length 1091;				
Best Local Similarity	76.5%; Pred. No. 1,2e-111;				
Matches	941; Conservative 19; Mismatches 44; Indels 226; Gaps 5;				
QY	999 GAGGACTGGCGGACAGCGCTGGCGGAGACACACGAGAGAGGCCAACCATCTTCTCCCTG 1055				
DB	1078 GRRGAGAGSTGGCGGAGGSGTCGGACACACAGAGAGCGAACACGATCTTCTGCGCTG 1015				
QY	1059 CGCAGAGACTTCGCCGAGGCGCAGGCCCGACGCTCCGGTGATGAGAGAGAGATG 1115				
DB	1018 SGCAAGAGACSTCCGCGCAGGCGAGGCCCGAC-SCTCGGGTGATGAGAGAGAGAGATG 960				
QY	1119 TTGAGCTGCACTGCTTGGCACTTACTGAAGACTCCAGATGTACAAGACCGCATCGAG 1177				
DB	959 TTGAGCTGCACTGCTTGGCA--TACGTAAGACTCCAGATGTACAAGACCGCATCGAG 902				
QY	1179 GCCATCTGCTGCACATGAGAGAGGTCCGCACTTGAAGCGGACCAAGAGACCAAAATGAG 1233				
DB	901 GCCATCTGCTGCACATGAGAGAGGTCCGCACTTGAAGCGGAC-- 860				
QY	1239 GGGCTGTACACAGCTCCGCGGCCACAGCGGCTTGAGTGCTCCCGAGAGCCTCTGCTGAGT 1295				
DB	859 ----- 860				
QY	1299 TGGGCGGCCGGGCGAGAGGCCAGAGGACCAAGCTTGGGGCCCTCATTGAGGCTCGCCTTGT 1355				
DB	859 ----- 860				
QY	1359 GCTGTGCTCCGTCAAGGCTATGACACGCGGAGAGAGCTGCACGACACAGAGCCCCGGGGCT 1411				
DB	859 -----CAGGCTATGACGACGCGGAGATTGTTTTCACGACACGACGAGCCCCGGGGCT 810				

[illegible]

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov

Plate: L1M1538 row: F column: 15
 High quality sequence stop: 9
 High quality sequence start: 732.
 Location/Qualifiers

FEATURES

Source

1..738
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5214350"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_118"
 /note="Vector: PCMV-SPT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

BASE COUNT

151 a 225 c 243 g 119 t

ORIGIN

Query Match 29.7%; Score 645.6; DB 12; Length 738;
 Best Local Similarity 97.5%; Pred. No. 8.7e-111;
 Matches 698; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

24 CCGGCGGCTCTCCCTCCCTCCGAGAGCCCGGAGAGATCTCCAGAGAGCTCCGCGGCCA 83
 23 CGGTCGTCT 82
 84 GGC-TCTGTGTGTGTCTGAGTGA-GGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 141
 83 GGGCTCTGTGTGTGTCTGAGTGAAGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 142
 142 AGGCTATGTGTGTGTCTGAGTGAAGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 201
 143 AGGCTATGTGTGTGTCTGAGTGAAGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 202
 202 TGAAGCTCACTGT 261
 203 TGAAGCTCACTGT 262
 262 TCTCTGAGAGCTGT 321
 263 TCTCTGAGAGCTGT 322
 322 GGAAGT 381
 323 GGAAGT 382
 382 TCTCTGAGAGCTGT 441
 383 TCTCTGAGAGCTGT 442
 442 CGGCGCGCT 501
 443 CGGCGCGCT 502
 502 TGAATGATGAGGTATGAGCTGAGAAAGGTGAGGAGCTGAGCCGCTCTGAGCT 561
 503 TGAATGATGAGGTATGAGCTGAGAAAGGTGAGGAGCTGAGCCGCTCTGAGCT 562

QY

562 CCAAGATGATCTTATCAAGAGAGCTGCGGTGAAAGACAGAGCTGTGCGAAGACAGG 621

Db

563 CCAAGATGATCTTATCAAGAGAGCTGCGGTGAAAGAGAGCTGTGCGAAGACAGG 622

QY

622 AGCGTGTGAGAGAGCTCAA-GGAGAGTGCAGAGCGCGAGCCGAGCTCAAGCGCTGC 680

Db

623 AGCGTGTGAGAGAGCTCAAAGGAGAGAGTGCAGAGCGCGAGCTCAAGCGCTGC 682

QY

681 AAGAGAGAGAA-CTACGACCTTGCCATGCGCTGCGCAGCAAGTGAAGAGAGG 735

Db

683 ACGGAGAGAGAACTACGACCTTGCCATGCGCTGCGCAGCAAGTGAAGAGG 738

RESULT 10

BF307399 829 bp mRNA linear EST 21-NOV-2000
 LOCUS 601894035F1.NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139529 5',
 DEFINITION mRNA sequence.

ACCESSION

BF307399

VERSION

BF307399.1 GI:11254514

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

TITLE

Unpublished

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

FEATURES

Location/Qualifiers

Source

1..829
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4139529"
 /tissue_type="rhabdomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_17"
 /note="Organ: muscle; Vector: pOT87; Site 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAC(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

173 a 249 c 279 g 128 t

ORIGIN

Query Match 29.2%; Score 636.2; DB 10; Length 829;
 Best Local Similarity 91.5%; Pred. No. 5.1e-109;
 Matches 707; Conservative 0; Mismatches 63; Indels 3; Gaps 3;

QY

6 CAGAAGTGCACAGAGCTCCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 65

Db

2 CAGAAGTGCACAGAGCTCCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60

QY

66 CAGAAGTCTCCGCGCTCCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125

Db

61 CAGAAGTCTCCGCGCTCCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 119

QY

126 CTCAGCTGCTGCTGAGGCAATGCGACTACGAGAAAGATGAGAGTGTGGAAGCTC 185

```

Db      120 CTGACGCTGCTGCTGCTGAGGCCATGTGCGACTACGAGAACATGACGAGTGTGAGAGCTC 179
QY      186 CTGAGAGGCTTCCGGGTGAGCGCTCACTCGGTGATGACCCCTACAGCATCACACCTTAC 245
Db      180 CTGAGAGGCTTCCGGGTGAGCGCTCACTCGGTGATGACCCCTACAGCATCACACCTTAC 239
QY      246 CTGCGGAGTGCAGAGGCTCTGAAACCTGATGATGAGAGAGAGGTGCTCAGCCACCCCAAC 305
Db      240 CTGCGGAGTGCAGAGGCTCTGAAACCTGATGATGAGAGAGAGGTGCTCAGCCACCCCAAC 299
QY      306 CTGCTCATCCGCAAGAGGAGAGTGGTGTCTCTGAGCATCTCTGAGAGGAGAGCCGGCCAC 365
Db      300 CTGCTCATCCGCAAGAGGAGAGTGGTGTCTCTGAGCATCTCTGAGAGGAGAGCCGGCCAC 359
QY      366 AAGGGCTACGCTGAGCTTCTCTGAGAGGCTGAGAGCTTACTACCCGAGCTGTACAGAG 425
Db      360 AAGGGCTACGCTGAGCTTCTCTGAGAGGCTGAGAGCTTACTACCCGAGCTGTACAGAG 419
QY      426 GTCAAGAGAGAGAGAGCCGCGCTTCTCTGATGATGATGATGATGATGATGATGATGATGAT 485
Db      420 GTCAAGAGAGAGAGAGCCGCGCTTCTCTGATGATGATGATGATGATGATGATGATGATGAT 479
QY      486 GGGCTGACTCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
Db      480 GGGCTGACTCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
QY      546 ACCGCGCTGCTGAGCTGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
Db      540 ACCGCGCTG- TGAGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 598
QY      606 CTGCGCAAGAGAGAGAGAGCTGCTGAGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
Db      599 GTGCGCAAGAGAGAGAGAGCTGCTGAGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 658
QY      666 GAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 725
Db      659 AGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718
QY      726 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 778
Db      719 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 771

```

```

RESULT 11
LOCUS      BM922630          1132 bp      mRNA      linear      EST 12-MAR-2002
DEFINITION AGENCOURT 6652616 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5755714
            5', mRNA sequence.
ACCESSION  BM922630
VERSION     BM922630.1  GI:19373009
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catartini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 1132)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL    Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cga@pds-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LHAM2795 row: c column: 11
            High quality sequence stop: 592.
            Location/Qualifiers

```

```

FEATURES
    source          1..1132
                    /organism="Homo sapiens"

```

```

/mo1_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5755714"
/tissue_type="Leukocyte"
/lab_host="MDH10B"
/clone_id="NIH_MGC_118"
/note="Vector: pCMV-SPORT6, Site_1: NotI, Site_2: EcoRV
(deleted); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invivo). Research Genetics tracking code 027. Note:
this is a NIH MGC Library."
BASE COUNT      243 a      363 c      331 g      195 t
ORIGIN

```

```

Query Match      28.6%; Score 621.4; DB 12; Length 1132;
Best Local Similarity 98.0%; Pred. No. 3.2e-106;
Matches 650; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

```

```

QY      44 TGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 103
Db      20 TGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 79
QY      104 TGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 163
Db      80 TGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 139
QY      164 CGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
Db      140 CGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 199
QY      224 CCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 283
Db      200 CCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259
QY      284 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
Db      260 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319
QY      344 CATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
Db      320 CATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 379
QY      404 CTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
Db      380 CTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 439
QY      464 CATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 523
Db      440 CATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 499
QY      524 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
Db      500 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 559
QY      584 GGTGGGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
Db      560 GGTGGGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 619
QY      644 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
Db      620 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 679
QY      702 GCC 704
Db      680 GGC 682

```

```

RESULT 12
BI837662

```

LOCUS B1837662 768 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603086501F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5225377 5',
 mRNA sequence.
 ACCESSION B1837662
 VERSION B1837662.1 GI:15949212
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NIH-MGC <http://mgs.nci.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1AM1567 row: b column: 02
 High quality sequence stop: 707.
 Location/Qualifiers
 1..768
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5225377"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_120"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 174 a 229 c 258 g 107 t

ORIGIN

Query Match 27.0%; Score 587.6; DB 12; Length 768;
 Best Local Similarity 94.4%; Pred. No. 6.2e-100;
 Matches 719; Conservative 0; Mismatches 29; Indels 14; Gaps 10;

QY 231 CGCATCACACCTTACTCTGGCGGAGTGCAAGTCTTGAACCTGTATGAGAGCAGGTG 290
 Db 1 CGCATCACACCTTACTCTGGCGGAGTGCAAGTCTTGAACCTGTATGAGAGCAGGTG 60
 QY 291 CTAGAGCAACCCCAACCTGTATCCGCAACGAAAGTGGTGTCTCTCGACATCTCG 350
 Db 61 CTAGAGCAACCCCAACCTGTATCCGCAACGAAAGTGGTGTCTCTCGACATCTCG 120
 QY 351 CAGGCGACCGGCAACGAGGCTACGTGGCTTCTCGAGAGCTGTACTACTACCG 410
 Db 121 CAGGCGACCGGCAACGAGGCTACGTGGCTTCTCGAGAGCTGTACTACTACCG 180
 QY 411 CAGCTGTACAGAAAGTTCACAGGCAAGAGCCGGCCGCTCTTCTCCATGATCATGAC 470
 Db 181 CAGCTGTACAGAAAGTTCACAGGCAAGAGCCGGCCGCTCTTCTCCATGATCATGAC 240
 QY 471 GCGTCCGGGAGTCAAGGCTGACTCAGCTGTGTATGACTAGAGTCATGAAGCTGCAAG 530
 Db 241 GCGTCCGGGAGTCAAGGCTGACTCAGCTGTGTATGACTAGAGTCATGAAGCTGCAAG 300
 QY 531 AAGGTG-CAGAGACTGACCGGCTGAGACTCCAAAGATGATCATCAAGAGCTGGG 589
 Db 301 AAGGTGCAAGAGACTGACCGGCTGAGACTCCAAAGATGATCATCAAGAGCTGGG 360

QY 590 GGTGAAGACAGCC-TGCTGCGCA-CCACACAGAGGCTGTGAGAGGCTCAAGAGGAG 647
 Db 361 GGTGAAGACAGCCAGCTTGCTGCTGCAATGACACAGAGGCTGTGAGAGGCTCAAGAGGAG 420
 QY 648 TCGAGAGCCGAGCA-GCCGAGAGCTCAAGCGCTGCAAGAGAGAACTACAGACTGGCCAT 706
 Db 421 TCGAGAGCCGAGCATGCGGAGAGCTCAAGCGCTGCAAGAGAGAACTACAGACTGGCCAT 480
 QY 707 GCGCTGCGGACACAGAGTGAAGAGAGAGGCGCGC-GCTCATGCGGA-CCGTGACCTG 764
 Db 481 GCGCTGCGGACACAGAGTGAAGAGAGAGGCGCGCGCTGCTCAAGCGGAACCCGTGACCTG 540
 QY 765 CAGCTGGAAGATTGACCAAGCTCAAGCAGCCTCTCATGAGGCCCGAGAGCACTGACAGT 824
 Db 541 CAGCTGGAAGATTGACCAAGCTCAAGCAGCCTCTCATGAGGCCCGAGAGCACTGCAAGGCT 600
 QY 825 GAGGCG-----AGCACAGCTGAAGCTCAGGCAC-GCCATGAGCA-GGGGCCACGCCA 877
 Db 601 GGAAGCCGACAGCAACAGCTGCAAGCTCAGGCACCGGCATGAGAGCGAGGACAGGCA 660
 QY 878 GGAGCTGTGTGGAGCTGCGAGAGAGAGAGGCGCTCTCAAGGCCCGGAGTGCAGAGCT 937
 Db 661 GGAGCTGTGTGGAGCTGCGAGAGAGAGAGGCGCTCTCAAGGCCCGGAGTGCAGAGCT 720
 QY 938 GAGAGCCTCCCTCCAGAGAGGAGGAGCTGCAAGAGAGAGGCC 979
 Db 721 GAGAGCCTCCCTCCA-GAGGAGAGCTGCAAGAGAGAGGCC 761

RESULT 13
 BG470298 728 bp mRNA linear EST 21-MAR-2001
 BG470298
 LOCUS 602533257F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660886 5',
 mRNA sequence.
 ACCESSION BG470298
 VERSION BG470298.1 GI:13402573
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NIH-MGC <http://mgs.nci.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1CM1459 row: a column: 15
 High quality sequence stop: 667.
 Location/Qualifiers
 1..728
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4660886"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_15"
 /note="Organ: colon; Vector: pOTB1; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

FEATURES
 source

QY 1580 ATGGCTCACCGAGAGGTCCAGAGCTCTCACTCCCGAGAGCTGAGAGCACCCAGC 1639
 Db 524 ATGGCTCACCGAGAGGTCCAGAGCTCTCACTCCCGAGAGCTGAGAGCACCCAGC 583
 QY 1640 TCTCAACAAAGGCTGCTTGGCGGCGGAGAGCCGAAACAGCCCTTTGAGCTTGC 1699
 Db 584 TCTCAACAAAGGCTGCTTGGCGGCGGAGAGCCGAAACAGCCCTTTGAGCTTGC 642
 QY 1700 ACCAGAGAGAGTGTGGCGGAGCCCGATGAGCGAGAGCTGAGAGCGGAGAGCCGCG 1759
 Db 643 ACCAGAGAGAGTGTGGCGGAGCCCGATGAGCGAGAGCTGAGAGCGGAGAGCCGCG 701
 QY 1760 AGAAGAGCGCGCGCCCTCAAAAGAGATTGAGAACTACCGAGAGAGCCGCGCTCA 1819
 Db 702 AGAAGAGCGCGCGCCCTCAAAAGAGATTGAGAACTACCGAGAGAGCCGCGCTC 761
 QY 1820 GGAAGATGCAAAAGATGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1864
 Db 762 AGAAGATGCAAAAGATGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 805

RESULT 15
 BX327160 940 bp mRNA linear EST 02-MAY-2003
 LOCUS BX327160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1039YL23 5-PRIME, mRNA sequence.

ACCESSION BX327160
 VERSION BX327160.1 GI:30346483
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. (bases 1 to 940)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5080.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BAF025ZB10.AF02379.3&cluster=5080.r.
 Contact: Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope Sequence ID: CS0BAF025ZB10.AF02379_3.
 Location/Qualifiers

FEATURES
 source

1. 940
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1039YL23"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="Left strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 202 a 293 c 331 g 112 t
 ORIGIN

Query Match 25.3%; Score 550.2; DB 13; Length 940;
 Best Local Similarity 81.0%; Pred. No. 6,4e-93;
 Matches 770; Conservative 0; Mismatches 25; Indels 156; Gaps 5;

QY 916 TCCAGGCGCGGAGAGAGCTGAGAGCTCCGTCAGAGAGAGAGAGAGAGAGAGAGAG 975
 Db 7 TCAAGTCCCGGATGCGAGAGCTGAGAGCTCCGTCAGAGAGAGAGAGAGAGAGAGAG 65

QY 976 GCCCTTACATCCAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1035
 Db 66 GCCCTTACATCCAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125
 QY 1036 AGGCGAACACCATTTCTCCCTGCGCAAGAGACCTCCGCAAGAGAGAGAGAGAGAGAG 1095
 Db 126 AGGCGAACACCATTTCTCCCTGCGCAAGAGACCTCCGCAAGAGAGAGAGAGAGAG 185
 QY 1096 GGTCAATGAG 1155
 Db 186 GGTCAATGAG 245
 QY 1156 AGATGTACAG 1215
 Db 246 AGATGTACAG 305
 QY 1216 GGGACAG 1275
 Db 306 GGGAC----- 310
 QY 1276 CCTCGAGAGCTCTGCTTGAGATTGGAGGCGCGGCGGAGAGAGAGAGAGAGAGAG 1335
 Db 311 ----- 310
 QY 1336 CCTCACTGAGAGTCCGCTTGTGCTGTCCTGTCAGAGAGAGAGAGAGAGAGAGAG 1395
 Db 311 -----CAGGCTATAGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 337
 QY 1396 CACGACAG 1455
 Db 338 CACGACAG 397
 QY 1456 CTGGGCGAG 1515
 Db 398 CTGGGCGAG 457
 QY 1516 GCCGTGAG 1575
 Db 458 GCCGTGAG 517
 QY 1576 GAAGTGGCTCACCCAGAGAGTCCAGAGAGTCTCACTCCCGAGAGAGAGAGAGAG 1635
 Db 518 GAAGTGGCTCACCCAGAGAGTCCAGAGAGTCTCACTCCCGAGAGAGAGAGAGAG 577
 QY 1636 CAGCTCTCAGCAAAAGGCTGCTTGGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 1695
 Db 578 CAGCTCTCAGCAAAAGGCTGCTTGGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 637
 QY 1696 CTGACCCAG 1755
 Db 638 CTGACCCAG 697
 QY 1756 CCGGAG 1815
 Db 698 CCGGAG 752
 QY 1816 CTCAGAGAGATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1866
 Db 753 CCGTCAAG 801

Search completed: February 23, 2004, 11:18:54
 Job time : 4591 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 09:51:41 ; Search time 146 Seconds
(without alignments)
6578,423 Million cell updates/sec

Title: US-10-032-159a-19
Perfect score: 2176
Sequence: 1 atcaccaggaagtcacacg.....aaacagcagcggtcaccgc 2176

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCOTS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132.8	6.1	9551	1	US-08-056-200-93 Sequence 93, Appl
2	132.8	6.1	9551	2	US-08-800-644-93 Sequence 93, Appl
3	101	4.6	3489	2	US-08-728-323A-1 Sequence 1, Appl
4	101	4.6	3489	4	US-09-298-568-1 Sequence 1, Appl
5	101	4.6	3489	4	US-09-410-399-1 Sequence 1, Appl
6	101	4.6	32207	2	US-08-770-379-20 Sequence 20, Appl
7	101	4.6	32207	4	US-08-757-669A-20 Sequence 20, Appl
8	101	4.6	32207	4	US-09-230-371A-20 Sequence 20, Appl
9	100.6	4.6	1926	4	US-09-249-585A-2 Sequence 2, Appl
10	100.6	4.6	1926	4	US-09-410-399-3 Sequence 3, Appl
11	100.6	4.6	2580	4	US-09-050-863-2 Sequence 2, Appl
12	100.6	4.6	2580	4	US-09-359-081-2 Sequence 2, Appl
13	100.6	4.6	5452	2	US-09-130-114-1 Sequence 1, Appl
14	100.6	4.6	8705	4	US-09-647-244A-14 Sequence 14, Appl
15	100.6	4.6	9600	4	US-08-910-647-1 Sequence 1, Appl
16	100.6	4.6	9600	4	US-09-620-925-1 Sequence 1, Appl
17	100.6	4.6	10596	1	US-07-884-811-15 Sequence 15, Appl
18	100.6	4.6	10596	1	US-07-885-971-15 Sequence 15, Appl
19	100.6	4.6	10596	1	US-08-087-783A-15 Sequence 15, Appl
20	100.6	4.6	10596	1	US-08-194-088B-15 Sequence 15, Appl
21	100.6	4.6	10596	2	US-08-194-087-15 Sequence 15, Appl
22	100.6	4.6	10596	5	PCT-US93-04648-15 Sequence 5, Appl
23	90	4.1	1185	3	US-09-023-339-3 Sequence 3, Appl
24	90	4.1	1260	3	US-09-023-173-5 Sequence 5, Appl
25	90	4.1	1308	3	US-09-023-173-10 Sequence 10, Appl
26	90	4.1	1308	3	US-09-023-339-6 Sequence 6, Appl
27	88.4	4.1	1995	1	US-08-425-069-3 Sequence 3, Appl

28	88.4	4.1	1995	2	US-08-317-844B-3	Sequence 3, Appl
29	87.2	4.0	2338	1	US-08-425-069-1	Sequence 1, Appl
30	87.2	4.0	2338	2	US-08-317-844B-1	Sequence 1, Appl
31	79.2	3.6	2277	1	US-08-676-867-5	Sequence 5, Appl
32	79.2	3.6	2277	1	US-08-676-867-5	Sequence 5, Appl
33	79.2	3.6	2277	2	US-09-098-487-5	Sequence 5, Appl
34	76.4	3.5	2793	1	US-08-209-747-1	Sequence 1, Appl
35	76.4	3.5	2793	1	US-08-458-298-1	Sequence 1, Appl
36	73.6	3.4	1926	4	US-09-249-585A-4	Sequence 4, Appl
37	73.6	3.4	1931	2	US-09-130-114-2	Sequence 2, Appl
38	67.2	3.1	2793	1	US-08-209-747-1	Sequence 1, Appl
39	67.2	3.1	2793	1	US-08-458-298-1	Sequence 1, Appl
40	63.8	2.9	5661	4	US-08-938-105-2	Sequence 2, Appl
41	63.2	2.9	756	1	US-08-642-255-50	Sequence 50, Appl
42	62.4	2.9	1310	4	US-09-047-288-1	Sequence 1, Appl
43	62.4	2.9	1310	4	US-08-802-191-1	Sequence 1, Appl
44	62.4	2.9	2180	3	US-09-286-904-23	Sequence 23, Appl
45	62.4	2.9	2180	4	US-09-640-101-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-056-200-93

Sequence 93, Application US/08056200
Patent No. 5616500

GENERAL INFORMATION:

APPLICANT: Steinert, Peter M.

APPLICANT: Lee, Seung-Chul

APPLICANT: Kim, In-Gyu

APPLICANT: Chung, Soo-Il

APPLICANT: Park, Sang-Chul

TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and

TITLE OF INVENTION: Methods of Using Same

NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/056,200

FILING DATE: 30-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pedrick, Michael F.

REGISTRATION NUMBER: 36,799

REFERENCE/DOCKET NUMBER: NIH054,001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 760-0404

TELEFAX: (714) 760-9502

INFORMATION FOR SEQ ID NO: 93:

SEQUENCE CHARACTERISTICS:

LENGTH: 9551 Base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1507..1644

FEATURE:

NAME/KEY: intron

LOCATION: 1645..2511
 NAME/KEY: CDS
 LOCATION: 2512..8070
 US-08-056-200-93

Query Match 6.1%; Score 132.8; DB 1; Length 9551;
 Best Local Similarity 46.9%; Pred. No. 6.1e-18;
 Matches 637; Conservative 0; Mismatches 692; Indels 29; Gaps 6;

QY 477 GGGGATCTAGGCTCTGAGCTGATGACTGAGTCTCATGAGTGTGAGAGAGAGG 536
 DB 3190 GAGGAGGAGAGAGAGTTCAGAACTTGAGCGGCAAGACTGAGAGAGAGCGCCAGAG 3249
 QY 537 CAGAGCTTGACCGCTGCTGAGCTTCAAAATGATCTTCAAGAGAGTTCGAGTGAAG 596
 DB 3250 GAGAGCTGAG 3309
 QY 597 GACAGCTGCTGCTGAG 656
 DB 3310 GAG 3369
 QY 657 GAG 716
 DB 3370 GAG 3429
 QY 717 CACAG 776
 DB 3430 CAG 3489
 QY 777 GACAG 836
 DB 3490 CAG 3549
 QY 837 ACAGCTGAG 896
 DB 3550 GAG 3609
 QY 897 GAG 956
 DB 3610 CAG 3669
 QY 957 GAG 1016
 DB 3670 GAG 3729
 QY 1017 CAG 1076
 DB 3730 CAG 3786
 QY 1077 GAG 1136
 DB 3787 GAG 3846
 QY 1137 GAG 1196
 DB 3847 GAG 3906
 QY 1197 GAG 1248
 DB 3907 GAG 3966
 QY 1249 GAG 1308
 DB 3967 GAG 4026
 QY 1309 GAG 1368
 DB 4027 GAG 4086
 QY 1369 GAG 1428
 DB 4087 GAG 4143

QY 1429 GAG 1488
 DB 4144 GAG 4203
 QY 1489 GAG 1542
 DB 4204 GAG 4263
 QY 1543 GAG 1602
 DB 4264 GAG 4323
 QY 1603 GAG 1655
 DB 4324 GAG 4383
 QY 1656 GAG 1713
 DB 4384 GAG 4443
 QY 1714 GAG 1773
 DB 4444 GAG 4503
 QY 1774 GAG 1811
 DB 4504 GAG 4541

RESULT 2
 US-08-800-644-93
 Sequence 93, Application US/08800644
 Patent No. 5958752
 GENERAL INFORMATION:
 APPLICANT: Steinert, Peter M.
 APPLICANT: Lee, Seung-Chul
 APPLICANT: Kim, In-Gyu
 APPLICANT: Chung, Soo-Il
 APPLICANT: Park, Sang-Chul
 TITLE OF INVENTION: Titchohyalin and Transglutaminase-3 and
 NUMBER OF SEQUENCES: 117
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, Sixteenth Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/800,644
 FILING DATE: 14-FEB-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/056,200
 FILING DATE: 30-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Fedick, Michael F.
 REGISTRATION NUMBER: 36,799
 REFERENCE/DOCKET NUMBER: NIH054,001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (714) 760-0404
 TELEFAX: (714) 760-9502
 INFORMATION FOR SEQ ID NO: 93:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9551 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1507..1644
 FEATURE:
 NAME/KEY: intron
 LOCATION: 1645..2511
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 2512..8070
 US-08-800-644-93

Query Match 6.1%; Score 132.8; DB 2; Length 9551;
 Best Local Similarity 46.9%; Pred. No. 6.1e-18;
 Matches 637; Conservative 0; Mismatches 692; Indels 29; Gaps 6;

QY 477 GGGGAGTCAGGCTGACTCAGCTGCTGATGATGAGTCACTGAGCTGCAAGAAAGAGTG 536
 DB 3190 GAGGAGAAAGAGAGCTACCGAAGCTGAGCGGCAAGAGCTGAGAGGAGCGCCAGAGAG 3249
 QY 537 CAGGACCTGACCGCGCTGCTGAGCTCAGAAAGATGACTTCACTCAAGAGAGCTGCGGGTGAAG 596
 DB 3250 GAAGAGAGAGAGAGCAAGAAAGCTGAGGCGCGAGAGCACTAAAGCGCAAGAGAGAG 3309
 QY 597 GAGACCTGCTGCGCAAGAGCAAGAGAGCTGTGTCAAGAGAGCTCAAGAGAGAGTCCAGGCG 656
 DB 3310 GAGAGGCGCAGAGAGAGAGAGAGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 3369
 QY 657 GAGAGCGCGAGCTCAAGCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 716
 DB 3370 GAGAGGCGCAG 3429
 QY 717 CACCAAGTAG 776
 DB 3430 CGCAG 3489
 QY 777 GACCAAGTAG 836
 DB 3490 CGGAG 3549
 QY 837 ACCGTGAAGCTCAGGAG 896
 DB 3550 GAGCAG 3609
 QY 897 CAGCAG 956
 DB 3610 CAGGTGAG 3669
 QY 957 GGGAGCTGAG 1016
 DB 3670 AGGCGCAG 3729
 QY 1017 CTGCGGAG 1076
 DB 3730 CAGCAG 3786
 QY 1077 GGGAG 1136
 DB 3787 GAG 3846
 QY 1137 GCACTAGTAG 1196
 DB 3847 AAG 3906
 QY 1197 GAG 1248
 DB 3907 GAG 3966
 QY 1249 CAGGCTCGGAG 1308

DB 3967 GAG 4026
 QY 1309 GGGCAG 1368
 DB 4027 AGGAG 4086
 QY 1369 CAGGCTATGAG 1428
 DB 4087 GAG 4143
 QY 1429 GAGGCTGCGAG 1488
 DB 4144 GAG 4203
 QY 1489 GTGTTCCAGTGTGAG 1542
 DB 4204 CGGAG 4263
 QY 1543 CAGCTGAG 1602
 DB 4264 CAGGAG 4323
 QY 1603 GAGCTCTCACTCCCGAG 1655
 DB 4324 GAGCTGCTGAG 4383
 QY 1656 CTTGCGGCGGAG 1713
 DB 4384 CAGGAG 4443
 QY 1714 TTGCGGAAAG 1773
 DB 4444 CTGAAG 4503
 QY 1774 CGCTCAAG 1811
 DB 4504 CAGGCTCGGAG 4541

RESULT 3

US-08-728-323A-1
 ; Sequence 1, Application US/08728323A
 ; Patent No. 5948676
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Yuan
 ; APPLICANT: Behenzky, Roy A.
 ; APPLICANT: Russo, James U.
 ; APPLICANT: Edelman, Isidore S.
 ; APPLICANT: Moore, Patrick S.
 ; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
 ; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
 ; TITLE OF INVENTION: Encoding Same And Uses Thereof
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/728,323A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678

Db	2109	GGATGAGCAGGAGCAGGATGAGCAGGACAGAGGATGACGACGAGTGA	2168
Qy	911	CTTCTCCAGGCCCGGGTGCAGAGCTGGAAGCCTCCGTCCAGAGGGGAAAGCTTGACAG	970
Db	2169	GCAGCAGCAGGATGAGCAGCAGCAGAGATGACAGCAGCAGCAGGATTGAGCAGCAGCA	2228
Qy	971	GAGCAGCCCTCAATCCAGGTACTGGAGGAAGATCGGGGAGAGGCGCTGCAGCACCA	1030
Db	2229	GCAGAGTGAAGCAGCAGCAGCAGATGAACAGAGCAGCAGAGGAGAGCAGAGCAGCAGCA	2288
Qy	1031	GGACGAGGCCCAACCAATCTTCTCCCTGCGCAAGAACTCCGACGAGCGAGGCCGACG	1090
Db	2289	GGACGACGAGCAGAGATTTAGAGAGCAGAGCAGAGCAAGATTA-----GAGGATCAGCA	2339
Qy	1091	CTTCGGGTGATGAGAGGAAGAAGATTTGAGCTGCAGCTGCAGCTTGCACTACGTAAGCA	1150
Db	2340	GCAGAGATTAGAGGACGAGCAGAGGATTTAGAGGAGCAGGAGCAGGAGTTAGAGAGCA	2399
Qy	1151	CTCCAGATGTACAAGACCCGCATGAGGCCATCTCTGCAATGGAAGAGGTGCGCAT	1210
Db	2400	GGACGAGGAGTTAGAGGAGCAGAGCAGAGGATTTAGAGGACGAGGACGAGGATTAGAGCA	2459
Qy	1211	TGAGCGGAGCCAGAGCACAACAAATGAGAGGGGCTGACACAGCTTCGCGGCCACGGCTT	1270
Db	2460	GCAGAGGACGAGAGTTTAGAGGACAGAGCAGAGATTA-GAGAGCAGGAGCAGAGATTAG	2518
Qy	1271	GACGTCCTCGGAGGCTCTGCTTGAAGTTGAGCGCGCGCGGCGCGAGGGGCCAGGGCCAAAGCT	1330
Db	2519	AGGAGCAGAGGTGAGAGGCAAGGACAGGAGGTGGAAGACAGAGAGCAGAGCAGAGAG	2578
Qy	1331	TGGGAGCCCTCACTAGAGGGTCGGCTTGTGCTGTCCCTCAGAGCCATAGCCACGCGGAGG	1390
Db	2579	AGCAGGAATTTAGAGAGGTGAGAGGACAGCAGAGCAGAGCAGAGAGAGAGAGAGCAGG	2638
Qy	1391	AGCTGCACGACAGCAGCGCCCGGCGCTGCAGAGGAAGAGCGCGCTGCGCAGCAGGTGC	1450
Db	2639	AGTTAGAGAGGTGGAAGAGCAGGAGAGGACAGGATTTAGAGAGGTGGAAGACAGGAG	2698
Qy	1451	GGAGAGTGGGCGAAGAGCGGATGAGCTGACAGCTGCAGGTITCCAGTGTAGGCGCAGC	1510
Db	2699	AGCAGGAGTTAGAGAGGTGGAAGAGCAGGAGCAGCAGGAGTTAGAGGAGGTGGAAGAGC	2758
Qy	1511	TACTGCGCTGGAAGGCGAGGCTCAGCGCGGACAGCAGCTGGAG	1551
Db	2759	AGGAGCAGCAGGAGGTGGAACAGCAGAGGACGAGACGCTG	2799

```

RESULT 5
US-09-410-399-1
: Sequence 1, Application US/09410399
: Patent No. 6482587
: GENERAL INFORMATION:
: APPLICANT: Robertson, Erle S.
: APPLICANT: Colter, Murray A.
: TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
: TITLE OF INVENTION: to Genomic Host DNA
: FILE REFERENCE: UM-03778
: CURRENT APPLICATION NUMBER: US/09/410,399
: CURRENT FILING DATE: 1999-10-01
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patentrin Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3489
: TYPE: DNA
: ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

```

Query March	4.6%	Score 101;	DB 4;	Length 3489;
Best Local Similarity	44.9%;	Pred. No. 1.2e-11;		
Matches 476;	Conservative 0;	Mismatches 575;	Indels 10;	Gaps 2;
QY	491	GACTCAGCTGCTGATGACTAGCGTCATTAAGCTGCGAAGGAGGCGACGACCTGACCGC	550	

Db	1749	GCACACAGAGGGGAGCCACAGACAGCGGGAGGCCACACAGACAGGATATGACGACGACAGGA	1808
Oy	551	GCTGCTGAAGCTCCAAAGATGATCTTACATCAAGAGAGCTCGGTTGAAGACAGAGCTCTGCG	610
Db	1809	TGAGCAGACAGAGGATAGAGCAGCAGCAGGATTGAGCAGCAGACAGGATAGAGCAGCAGGA	1868
Oy	611	CAAGCACCAGAGGCTGTGAGAGGGCTCAAGGAGGAGATGAGAGGGCCGCGCAGCCGCGAGCT	670
Db	1869	TGAGCAGACAGAGGATGAGCAGCAGCAGGATTGAGCAGCAGACAGGATAGCAGCAGCAGGA	1928
Oy	671	CAAGCGCTGCAAGAGGAGAACTTACGACTGAGCATTCGCTCGCGCAGCAGAGTGAAGA	730
Db	1929	TGAGCAGACAGAGGATGAGCAGCAGCAGGATTGAGCAGCAGACAGGATGAGCAGCAGGA	1988
Oy	731	GAAGAGCGCGCGCTCATGCGGAAACGGTGACTTGACGCTGAGATTGACCAAGCTCAAGCA	790
Db	1989	TGAGCAGACAGAGGATGAGCAGCAGCAGGATTGAGCAGCAGACAGGATGAGCAGCAGGA	2048
Oy	791	CAGGCTTATAGAGGCCAGAGACCACTGCAGAGTGAAGCGCAAGCAACGCTGAAGCTCAG	850
Db	2049	TGAGCAGACAGAGGATGAGCAGCAGCAGGATTGAGCAGCAGACAGGATGAGCAGCAGGA	2108
Oy	851	GCAAGCCATGAGAGAGCGGCCACAGCCAGAGCGTGTGGAGAGTTCAGCAGAGGAAGGC	910
Db	2109	GGATGACAGAGAGCAGAGATGAGCAGAGCAGACAGGATGAGCAGCAGAGTGAAGCA	2168
Oy	911	CTTGCTTCAGAGCCCGGCTGAGAGAGCTGAGAGCCCTCGTCCAGAGAGGGAAGCTGACAG	970
Db	2169	GCAACACACAGGATGAGCAGCAGCAGCAGGATTGAGCAGCAGACAGACAGGATGAGCAGCAGCA	2228
Oy	971	GAGCAGCCCTTACATCCAGGTACTGAGAGAGACTGCGCGCAGAGCGCTCGCGGACCA	1030
Db	2229	GCAAGATGAGCAGCAGCAGCAGGATGAACAGAGCAGCAGAGGAGCAGAGAGCAGCAGGA	2288
Oy	1031	GGAACCAAGCCCAACCACTCTTCTCCCTGCGCAGAGACTCCGCCAGGGCCAGGCCACAG	1090
Db	2289	GGACCAAGCAGAGGATTGAAGAGCAGAGCAGAGGATT-----GAGGATTCAGGA	2339
Oy	1091	CCTCGGCTGATGAGAGAGAGAGAGATGTTGAGCTCAGAGCTCGCTGCGCACTTACCTTAAGGA	1150
Db	2340	GCAAGAGTTTGAAGAGCAGAGGAGCTTTAGAGAGACAGAGGACAGGATTTAGAGAGCA	2399
Oy	1151	CTCCAGATGTACAAGACCGCACTCGAGGCCATCTGCTCAGATGAGAGAGGTGCGCAT	1210
Db	2400	GGACACAGAGTTAGAGGAGCAGAGCAGAGGTTTGAAGACAGAGGACAGGATTGAAGAGGA	2459
Oy	1211	TGAGCGGAGCCAGAGCAACAATTGAGGAGGCTGTGACCAAGCTTCGCGCCAGCGGCTT	1270
Db	2460	GCAAGACACAGAGTTTGAAGAGGACAGGAGCAGAGGATT--GAGGAGCAGAGAGAGGATTGAG	2518
Oy	1271	GAGCTCTCCGAGAGCCCTGCTTGGAATTTGGGCGGCGCGGCCGAGGGGCCACAGGCCAAGCT	1330
Db	2519	AGGACAGAGAGGTGGAAGACGCAAGCAGAGGTTGGAAGACAAAGACAGAGCAGAGGAAG	2578
Oy	1331	TGGGAGCCCTCACTGAGGGTCCGCTTGTGCTGTCCGTCAAGGCCATTAGCAGCGGGAGG	1390
Db	2579	AGCAGGAAATTGAGAGAGGTGAGAGACAAAGACAGAGCAGCAGAGGACAGAGGAGCAGAG	2638
Oy	1391	AGCTGCACGCAACAGCACGCCCGGGGCTGCAAGAGAAAGACGCGCTGCGCAGCAGGTTCC	1450
Db	2639	AGTTTAGAGAGAGTTGAAGACAGGAAGACAGAGGATTAGAGAGGTGAAAGACAGGAAG	2698
Oy	1451	GGAGAGCTGGGCGAGAAAGCGGATGAGCTGCAGCTGCAGGTGTTCCAGTGTAGGCGCAGC	1510
Db	2699	AGCAGGAGTTTAGAGAGAGTGGAAAGACAGAGCAGCAGGATTTGAAGAGGTGGAAGAGC	2758
Oy	1511	TACTGAGCGTGGAGGAGCGAGCTCAGGCGGACAGCAGCTGGAG	1551
Db	2759	AGGAGCAGAGAGGAGGTGAGACAGCAGAGGACGAGAGCGGTG	2799

RESULT 6
US-08-770-379-20/c

APPLICATION NUMBER: US/08/757,669A
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 45185-F
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32207 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-757-669A-20

Query Match 4.6%; Score 101; DB 3; Length 32207;
 Best Local Similarity 44.9%; Pred. No. 1.9e-11;
 Matches 476; Conservative 0; Mismatches 575; Indels 10; Gaps 2;

491 GACTCAGCTGCTGATGATGAGTCTGAGTCAATGAAAGTGCAGAGACCTGACCGC 550
 20248 GCCACACAGCGGGAGCCAGCAGCGGAGCCACACAGCAGATGACAGCAGCAGGA 20189
 551 GCTCTAGCTCCAAAGATGATCTTATCAAGAGCTCGGGTGAAGAGCAGCTGTGCG 610
 20188 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGGA 20129
 611 CAAGCAGCAGAGAGCTGTGAGAGCTCAAGAGAGTGCAGAGCCGCGCAGAGCT 670
 20128 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGGA 20069
 671 CAAGCCTGCAAGAGAGAACTGACCTGCGCCATGCGCTGGCCGACCAAGATGAGA 730
 20068 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGCAGATGACAGCAGGA 20009
 731 GAAGGGGCGCGCTCATGCGGAACCGTGAAGCTGAGCTGAGATGACAGCTCAAGCA 790
 20008 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGCAGATGACAGCAGGA 19949
 791 CAGCTCATGAAGCCGAGAGCAGCTCAAGTGTGAGCGCAGACCAACGCTGAAGCTCAG 850
 19948 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGCAGATGACAGCAGGA 19889
 851 GCAAGCCATGAGAGAGCGCCAGCAGAGCTGCTGTGAGCTGAGAGCTGAGAGAGGC 910
 19888 GATGAGCAGAGAGCAGAGATGACAGCAGCAGATGACAGCAGCAGATGAGCA 19829
 911 CCTGCTCAAGGCCCGGCTGAGAGCTGAGAGCTCCGTCAGAGAGGGAGCTGAGCAG 970
 19828 GAGCAGCAGAGATGACAGCAGCAGCAGATGACAGCAGCAGCAGATGACAGCAGGA 19769
 971 GAGAGGCCCTCAATCATGAGGATCTGAGAGAGGACTGCGCGCAGAGCGCTGAGAGCA 1030
 19768 GAGAGATGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGAGAGAGCAGGA 19709
 1031 GAGCAGCAGCAGCAGCAGATCTTCTCCCTGCGCAAGAGCCTCGCAGAGGCGCCGAGC 1090
 19708 GAGCAGCAGCAGAGATGACAGCAGCAGCAGCAGATGACAGCAGCAGATGAGCA 19658
 1091 CTTCCGCTGATGAGAGAGAGAGATGTTGAGCTGCAAGTGCCTGCACTACGTAAGA 1150
 19657 GAGAGATGAGAGAGAGAGAGAGATGAGAGCAGCAGCAGAGATGAGAGAGCA 19598
 1151 CTCCAAATGTACAGAGAGCAGATGAGAGCAGATCTTCTGCAATGAGAGAGCTCGCAT 1210
 19597 GAGAGCAGAGATGAGAGAGCAGAGCAGATGAGAGAGCAGAGAGAGAGAGAGGA 19538
 1211 TGAGCGGAGCAGAGCAGCAGATGAGAGAGAGCTGAGCAGAGCTCGCGCGCCAGAGGCTT 1270

19537 GCAGAGCAGAGATGAGAGCAGAGCAGAGATTA-GAGAGCAGAGCAGAGATTAG 19479
 1271 GACGTCTCCGAGAGCTCTGCTTGAAGTTGGCGCGCCGAGAGGCCCAAGGAACT 1330
 19478 AAGAGCAGAGAGTGAAGAGCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19419
 1331 TGGGGCCCTCACTGAGAGGTCGCTTGTGCTGCTCCGTCAGAGCAGCAGCGGAGAG 1390
 19418 AAGAGAGATTAAGAGAGGTTGAGAGCAGAGCAGAGAGCAGAGAGAGAGAGAGAG 19359
 1391 AGCTGACGACAGACAGCAGCGCCGCGGCTGACAGAGAGAGCAGCGCTGCGCAGCAGTGC 1450
 19358 AGTTAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19239
 1451 GGAAGCTGGGCGAGAGAGCGGATGAGCTGACAGCTCAGAGTGTTCAGTGTGAGCGCAGC 1510
 19298 ACAGAGAGTTAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 19239
 1511 TACTGCGCTGAGAGGAGCAGAGCTCAGCGCGCAGCAGCTGAG 1551
 19238 AAGAGCAGAGGAGGAGTGAAGCAGAGCAGAGCAGAGAGAGAGAGAGAGAGAG 19198

RESULT 8
 US-09-230-371A-20/C
 ; Sequence 20, Application US/09230371A
 ; Patent No. 6348586
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Yuan
 ; APPLICANT: Bohenzky, Roy A
 ; APPLICANT: Russo, James J
 ; APPLICANT: Edelman, Isidore S
 ; APPLICANT: Moore, Patrick S
 ; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
 ; FILE REFERENCE: 45185-G-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/230,371A
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: PCT/US97/13346
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 32207
 ; TYPE: DNA
 ; ORGANISM: Kaposi's sarcoma-associated herpesvirus
 US-09-230-371A-20

Query Match 4.6%; Score 101; DB 4; Length 32207;
 Best Local Similarity 44.9%; Pred. No. 1.9e-11;
 Matches 476; Conservative 0; Mismatches 575; Indels 10; Gaps 2;

491 GACTCAGCTGCTGATGATGAGTCTGAGTCAATGAAAGTGCAGAGACCTGACCGC 550
 20248 GCCACAGCAGCGGGAGCCACAGCAGCGGAGCCACACAGCAGATGACAGCAGCAGGA 20189
 551 GCTCTAGCTCCAAAGATGATCTTATCAAGAGCTCGGGTGAAGAGCAGCTGTGCG 610
 20188 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGGA 20129
 611 CAAGCAGCAGAGAGCTGTGAGAGCTCAAGAGAGTGCAGAGCCGCGCAGAGCTGAGGA 730
 20128 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGGA 20069
 671 CAAGCCTGCAAGAGAGAACTGACAGCTGCGCCTGCGCGCAGAGAGTGAAGA 790
 20068 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGGA 20009
 731 GAAGGGGCGCGCTCATGCGGAACCGTGAAGCTGAGCTGAGATGACAGCTCAAGCA 790
 20008 TGAGCAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGATGACAGCAGCAGGA 19949
 791 CAGCTCATGAAGCCGAGAGCAGCTGCAAGTGTGAGCGCAGAGCAGCAGCTGAAGCTCAG 850


```

QY 528 AAGAGGTGACGAGACCTGACCGCTGTGAGCTCCAAAGATGACTTTCATCAAGAGCTG 587
DB 416 CAGAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475
QY 588 CGGGTGAAGACAGACCTGTGTGCGCAAGACACAGAGACCTGTGTCAAGAGCTCAAGAGAG 647
DB 476 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535
QY 648 TGGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 707
DB 536 GAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
QY 708 CGCTTGGCCGACCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 767
DB 596 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
QY 768 CTGAGATTGACACAGCTCAAGACACAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 827
DB 656 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 715
QY 828 CGCAGACACACGCTGAAGCTCAGGCAAGCATTGAGAGAGAGAGAGAGAGAGAGAGAG 887
DB 716 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 775
QY 888 TGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947
DB 776 GAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 835
QY 948 GTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1007
DB 836 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 895
QY 1008 CGGAGAGCGCTGCGGAGCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
DB 896 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 926

```

RESULT 11

US-09-050-863-2

Sequence 2, Application US/09050863

Patent No. 611411

GENERAL INFORMATION:

APPLICANT: Lao, Yang

APPLICANT: Hiang, Betty

APPLICANT: Payan, Don

TITLE OF INVENTION: Mammalian Protein Interaction Cloning

TITLE OF INVENTION: System

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flehr, Hobach, Test, Albrighton & Herbert

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050, 863

FILING DATE: 30-MAR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-65638/DJ/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 949-8711

INFORMATION FOR SEQ ID NO: 2:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-09-050-863-2

```

```

Query Match 4.6%; Score 100.6; DB 3; Length 2580;
Best Local Similarity 48.5%; Pred. No. 1.4e-11;
Matches 277; Conservative 0; Mismatches 294; Indels 0; Gaps 0;

```

```

QY 468 GAGCGGTCCGGGAGTACAGGCTGAGCTGATGACTGAGAGCTGATGAGAGCTGAG 527
DB 739 GAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798
QY 528 AAGAGGTGACGAGACCTGACCGCTGTGAGCTCCAAAGATGACTTTCATCAAGAGAGCTG 587
DB 799 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858
QY 588 CGGGTGAAGACAGACCTGTGTGCGCAAGACACAGAGACCTGTGTCAAGAGCTCAAGAGAGAG 647
DB 859 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
QY 648 TGGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 707
DB 919 GAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
QY 708 CGCTTGGCCGACCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 767
DB 979 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
QY 768 CTGAGATTGACACAGCTCAAGACACAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 827
DB 1039 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
QY 828 CGCAGACACACGCTGAAGCTCAGGCAAGCATTGAGAGAGAGAGAGAGAGAGAGAGAG 887
DB 1099 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
QY 888 TGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947
DB 1159 GAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
QY 948 GTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1007
DB 1219 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278
QY 1008 CGGAGAGCGCTGCGGAGCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
DB 1279 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1309

```

RESULT 12

US-09-359-081-2

Sequence 2, Application US/09359081

Patent No. 6316223

GENERAL INFORMATION:

APPLICANT: Lao, Yang

APPLICANT: Hiang, Betty

APPLICANT: Payan, Don

TITLE OF INVENTION: Mammalian Protein Interaction Cloning

TITLE OF INVENTION: System

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flehr, Hobach, Test, Albrighton & Herbert

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

Tue Feb 24 09:52:04 2004

us-10-032-159a-19.rml

Page 12

Search completed: February 23, 2004, 13:33:16
Job time : 151 secs

QY 121 AGACCTCAGCCTGCTGAGGCGATGTCGACCTACAGAGACGATGACGAGTCTGA 180
Db 121 AACCTCAGCCTGCTGAGGCGATGTCGACCTACAGAGACGATGACGAGTCTGA 180
QY 181 AGCTCTGAGAGGCTTCCGGGTGACGCTGACCTCGGTGATCGACCTCAGCATCAC 240
Db 181 AGCTCTGAGAGGCTTCCGGGTGACGCTGACCTCGGTGATCGACCTCAGCATCAC 240
QY 241 CTTACCTGCGGAGTGCAGAGGTCCTGAACCTGATGATGAGAGAGAGTGTCTCAGCGAC 300
Db 241 CTTACCTGCGGAGTGCAGAGGTCCTGAACCTGATGATGAGAGAGAGTGTCTCAGCGAC 300
QY 301 CCAACTGTGATCCGCGAAGCGAAAGTGTGTCTCTGACATCTCTGACGCGGACCG 360
Db 301 CCAACTGTGATCCGCGAAGCGAAAGTGTGTGTCTCTGACATCTCTGACGCGGACCG 360
QY 361 GCGACAGAGGCTACGAGGCTTCTCTGAGAGGCTGAGGCTGACCTGACCTGACCTGAC 420
Db 361 GCGACAGAGGCTACGAGGCTTCTCTGAGAGGCTGAGGCTGACCTGACCTGACCTGAC 420
QY 421 AGAAGCTCAGGCGAGAGAGCGCGCGCTTCTCTGATGATGATGATGATGATGATGATG 480
Db 421 AGAAGCTCAGGCGAGAGAGCGCGCGCTTCTCTGATGATGATGATGATGATGATGATG 480
QY 481 AGTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 481 AGTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 ACCTGACCGGCTGCTGAGTCTCAAGATGATGATGATGATGATGATGATGATGATG 600
Db 541 ACCTGACCGGCTGCTGAGTCTCAAGATGATGATGATGATGATGATGATGATGATG 600
QY 601 GCGTGTGCGGAG 660
Db 601 GCGTGTGCGGAG 660
QY 661 GCGCGAGCTCAGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 GCGCGAGCTCAGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 AGAGTGAAG 780
Db 721 AGAGTGAAG 780
QY 781 AGCTCAAGCAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 AGCTCAAGCAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 TGAAGCTCAG 900
Db 841 TGAAGCTCAG 900
QY 901 AG 960
Db 901 AG 960
QY 961 AGCTGAGCAG 1020
Db 961 AGCTGAGCAG 1020
QY 1021 GGGAGCAG 1080
Db 1021 GGGAGCAG 1080
QY 1081 AGGCGGAG 1140
Db 1081 AGGCGGAG 1140
QY 1141 TAGGTGAAG 1200
Db 1141 TAGGTGAAG 1200
QY 1201 AGGTGCGCATTTAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

Db 1201 AGGTGCGCATTTAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 CCAAGGCTTGAAGCTCTCCGAGAGCTTGTGAGATGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 CCAAGGCTTGAAGCTCTCCGAGAGCTTGTGAGATGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 AGGCGAAGCTTGGAG 1380
Db 1321 AGGCGAAGCTTGGAG 1380
QY 1381 AGCGGAG 1440
Db 1381 AGCGGAG 1440
QY 1441 AAGCAGGCTGAG 1500
Db 1441 AAGCAGGCTGAG 1500
QY 1501 GAGCGAG 1560
Db 1501 GAGCGAG 1560
QY 1561 CTGAGCTCCGAGCTGAG 1620
Db 1561 CTGAGCTCCGAGCTGAG 1620
QY 1621 GACCTGAG 1680
Db 1621 GACCTGAG 1680
QY 1681 CAGCCCTTGAAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 CAGCCCTTGAAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 AGCAGCGGAG 1800
Db 1741 AGCAGCGGAG 1800
QY 1801 CCGAG 1860
Db 1801 CCGAG 1860
QY 1861 GAG 1920
Db 1861 GAG 1920
QY 1921 CCGAGCGCTGCTGAG 1980
Db 1921 CCGAGCGCTGCTGAG 1980
QY 1981 ACTGCGGAG 2040
Db 1981 ACTGCGGAG 2040
QY 2041 CTGACAG 2100
Db 2041 CTGACAG 2100
QY 2101 TAAACAG 2160
Db 2101 TAAACAG 2160
QY 2161 AGCAGGAG 2176
Db 2161 AGCAGGAG 2176

QY	1765	GAGCGGCGGCGCCCTCAAGAGAGTTTGAACA	CTCCGACAGAAAGCGGCGCTCAGAGAG	1824
Db	1614	GAGCGGCGGCGCCCTCAAGAGAGTTTGAACA	CTCCGACAGAAAGCGGCGCTCAGAGAG	1673
QY	1825	ATGCAGAAAGATGCGCGGACAGGGAGAGAGA	CCGGGAGAAACCAACCGGGACGCGACAC	1884
Db	1674	ATGCAGAAAGATGCGCGGACAGGGAGAGAGA	CCGGGAGAAACCAACCGGGACGCGACAC	1733
QY	1885	ACCGA	CTGAGGGCTCCTAGCCGCA-----	1910
Db	1734	ACCGA	CTGAGGGCTCCTAGCCGCAAGGCCGACACCA	1733
QY	1911	-----	CCAGACTTCCCCGAGCCGTCCT	1933
Db	1794	CCCGGCTGCACCCCGGGGTGCGCAGCCCT	GGGGCCGACACTTCCCGAGCCGTCCT	1853
QY	1994	GACTTGGCTGGAGACGAGAAATCTGTGTGCT	GTGAGAAAGGCCGACGCTGCGGGCAAT	1993
Db	1854	GACTTGGCTGGAGACGAGAAATCTGTGTGCT	GTGAGAAAGGCCGACGCTGCGGGCAAT	1913
QY	1994	GGGGCGCTTTGTTTAAAGCGGCACTATTTT	GCGAGGCCATGCGGGTGTCTACACCCCA	2053
Db	1914	GGGCGCTTTGTTTAAAGCGGCACTATTTT	GCGAGGCCATGCGGGTGTCTACACCCCA	1973
QY	2054	TGCACAGCCCATCTGTGTACTTCCAGATCT	GTGTCTGTTTCCATCATGTAAACACAAATAC	2113
Db	1974	TGCACAGCCCATCTGTGTACTTCCAGATCT	GTGTCTGTTTCCATCATGTAAACACAAATAC	2033
QY	2114	ATGCATGATGTGTATTAGTGT-TAGAAACAC	ACGCTGCTAATTAACAGACAGGGGTAC	2172
Db	2034	ATGCATGATGTGTATTAGTGTAAAGAAACAC	ACGCTGCTAATTAACAGACAGGGGTAC	2033
QY	2173	CCGC	2176	
Db	2094	CCGC	2097	
RESULT 3				
US-10-325-917-4				
; Sequence 4, Application US/10325917				
; Publication No. US20030113787A1				
; GENERAL INFORMATION:				
; APPLICANT: Berlin, John				
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED				
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF				
; FILE REFERENCE: 07334-327001				
; CURRENT FILING DATE: 2002-12-20				
; PRIOR APPLICATION NUMBER: US/09/798,412				
; PRIOR FILING DATE: 2001-03-02				
; PRIOR APPLICATION NUMBER: US 09/728,260				
; PRIOR FILING DATE: 2000-12-01				
; PRIOR APPLICATION NUMBER: US 09/685,791				
; PRIOR FILING DATE: 2000-10-10				
; PRIOR APPLICATION NUMBER: US 09/513,904				
; PRIOR FILING DATE: 2000-02-25				
; PRIOR APPLICATION NUMBER: US 09/507,533				
; PRIOR FILING DATE: 2000-02-18				
; PRIOR APPLICATION NUMBER: US 60/168,780				
; PRIOR FILING DATE: 1999-12-03				
; NUMBER OF SEQ ID NOS: 19				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO: 4				
; LENGTH: 2098				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (144)...(1751)				
US-10-325-917-4				
Query Match	80.2%	Score 1746,	DB 15,	Length 2098;

[illegible]

Db 421 GATGACTTCAATCAGAGAGCTGCGGGTGAAGAGACAGCTGCTGCGCAAGCAACAGAGCT 480
QY 627 GTGCAGAGGCTCAAGAGAGAGTGCAGAGCGCGAGCGCGAGGCTCAAGAGCTGCAAGAG 686
Db 481 GTGCAGAGGCTCAAGAGAGAGTGCAGAGCGCGAGCGCGAGGCTCAAGAGCTGCAAGAG 540
QY 687 GAGAACTACAGCTGCGCATGCGCTCGCGCACAGAGTGAAGAGAGAGGCGCGCGCTC 746
Db 541 GAGAACTACAGCTGCGCATGCGCTCGCGCACAGAGTGAAGAGAGAGGCGCGCGCTC 600
QY 747 ATGCGGAACCGTGAAGCTGCGAGCTGAGAGATTGACCACTCAAGAGACGCTCATGAGAGCC 806
Db 601 ATGCGGAACCGTGAAGCTGCGAGCTGAGAGATTGACCACTCAAGAGACGCTCATGAGAGCC 660
QY 807 GAGAGCACTGCAAGAGTGAAGCGCAAGCAACGCTGAAGTCAAGAGCGCAATGAGAGAG 866
Db 661 GAGAGCACTGCAAGAGTGAAGCGCAAGCAACGCTGAAGTCAAGAGCGCAATGAGAGAG 720
QY 867 CGGCGCAAGCAGAGAGCTGCTGTGAGAGCTGCAAGAGAGAGAGCCCTGCTCAAGAGCCCG 926
Db 721 CGGCGCAAGCAGAGAGCTGCTGTGAGAGCTGCAAGAGAGAGAGCCCTGCTCAAGAGCCCG 780
QY 927 GTGCAGAGAGCTGAGAGGCTTCCGTTCAGAGAGAGAGAGCTGCAAGAGAGAGAGAGAG 986
Db 781 GTGCAGAGAGCTGAGAGGCTTCCGTTCAGAGAGAGAGAGAGCTGCAAGAGAGAGAGAG 840
QY 987 CAGGTAATGAG 1046
Db 841 CAGGTAATGAG 900
QY 1047 ATCTCTCCCTGCGCAAGAGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1106
Db 901 ATCTCTCCCTGCGCAAGAGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 1107 GAG 1166
Db 961 GAG 1020
QY 1167 GAGCGCATGAG 1226
Db 1021 GAGCGCATGAG 1074
QY 1227 ACACAAATGAG 1286
Db 1075 ----- 1074
QY 1287 TGTGCTTGAAGTTGGGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1346
Db 1075 ----- 1074
QY 1347 GGTGCGGCTTGTGCTGTCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1406
Db 1075 -----CAGGCGATAGCAAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1112
QY 1407 CGGCGCGGCGCTGAG 1466
Db 1113 CGGCGCGGCGCTGAG 1172
QY 1467 GGGCGATGAGAGCTGAG 1526
Db 1173 GGGCGATGAGAGCTGAG 1232
QY 1527 CAGGCTCAG 1586
Db 1233 CAGGCTCAG 1292
QY 1587 ACCGAG 1646
Db 1293 ACCGAG 1352
QY 1647 CAAAG 1706
Db 1353 CAAAG 1412

QY 1707 GCAGGTTTTCGGAACCCCATGAGCAGAGCTTGAGAGCGGAGAGAGAGAGAGAGAGAGAGAG 1766
Db 1413 GCAGGTTTTCGGAACCCCATGAGCAGAGCTTGAGAGCGGAGAGAGAGAGAGAGAGAGAGAG 1472
QY 1767 GCGGCGGCGCTCAAGAGAGAGTTTGAAGACTACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1826
Db 1473 GCGGCGGCGCTCAAGAGAGAGTTTGAAGACTACCGAGAGAGAGAGAGAGAGAGAGAGAG 1532
QY 1827 GCAGAAAG 1886
Db 1533 GCAGAAAG 1592
QY 1887 CGACACTGAGAGAGCTCC 1902
Db 1593 CGACACTGAGAGAGCTCC 1608

RESULT 5
US-10-325-917-6
; Sequence 6, Application US/10325917
; Publication No. US20030113787A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 0734-327001
; CURRENT APPLICATION NUMBER: US/10/325,917
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/09/798,412
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-917-6

Query Match 66.6%; Score 1448.4; DB 15; Length 1608;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1607; Conservative 0; Mismatches 1; Indels 148; Gaps 1;

QY 147 ATGTGGAAGTACGAG 206
Db 1 ATGTGGAAGTACGAG 60
QY 207 CTACCTCGCTCATGAG 266
Db 61 CTACCTCGCTCATGAG 120
QY 267 AACCTGATGATGAG 326
Db 121 AACCTGATGATGAG 180
QY 327 GTGGGTGTGCTTCCTGAG 386
Db 181 GTGGGTGTGCTTCCTGAG 240
QY 387 GAGAGCTGAGAGCTTACTACCGAG 446
Db 241 GAGAGCTGAGAGCTTACTACCGAG 300

QY	387	GAGAGCGCTGAGGCTCTACTACCCCGAGGCTGTAACAAGAGGCTCACAGGCAAGAGCCGGCC	446
Db	241	GAGAGGCTTGAGGCTCTTACTACCCGAGGCTGTACAAAGAGGCTCACAGGCAAGAGCCGGCC	300
QY	447	CGCGTCTTCTTCATGATCATCGAGCGGCTCCGGGAGTCCAGGCTTGACTCAGCTGCTATG	506
Db	301	CGCGTCTTCTTCATGATCATCGAGCGGCTCCGGGAGTCCAGGCTTGACTCAGCTGCTATG	360
QY	507	ACTGAGGTCATGAAGCTGCAAGAAGGTGCAGAGCTGACCCGGCTGCTGACTCCAA	566
Db	361	ACTGAGGTCATGAAGCTGCAAGAAGGTGCAGAGCTGACCCGGCTGCTGACTCCAA	420
QY	567	GATGACTTCATCAAGAGAGCTCGGGTGAAGACAGGCTGCTGGCAACACAGAGAGCT	626
Db	421	GATGACTTCATCAAGAGAGCTCGGGTGAAGACAGGCTGCTGGCAACACAGAGAGCT	480
QY	627	GTGCAAGAGGCTCAAGAGAGAGTGCAGAGCCGGACCCGACCTCAAGCGCTGCAGAGAG	686
Db	481	GTGCAAGAGGCTCAAGAGAGAGTGCAGAGCCGGACCCGACCTCAAGCGCTGCAGAGAG	540
QY	687	GAGAACTACGACTTGCGCATCGCTGCGACACAGAGTGAAGAGAGCGCGCTC	746
Db	541	GAGAACTACGACTTGCGCATCGCTGCGACACAGAGTGAAGAGAGCGCGCTC	600
QY	747	ATGCGGAACCGTGACCTTGACCTGAGAGTTGACCAAGCTCAAGCACAGCTTATGAAGCC	806
Db	601	ATGCGGAACCGTGACCTTGACCTGAGAGTTGACCAAGCTCAAGCACAGCTTATGAAGCC	660
QY	807	GAGAGCGACTGCAAGGTGAGGCGCAAGACACGCTGAAGCTCAGGACAGCCATGAGAG	866
Db	661	GAGAGCGACTGCAAGGTGAGGCGCAAGACACGCTGAAGCTCAGGACAGCCATGAGAG	720
QY	867	CGGCCCAACCGCAGAGGCTGCTGAGAGCTGAGCAGAGAGGCGCTGCTCAAGCCCGG	926
Db	721	CGGCCCAACCGCAGAGGCTGCTGAGAGCTGAGCAGAGAGGCGCTGCTCAAGCCCGG	780
QY	927	GTGCAAGAGCTGAGAGGCTTCCGCTCCAGAGAGGAGAGCTTGACAGAGAGCCCTTACATC	986
Db	781	GTGCAAGAGCTGAGAGGCTTCCGCTCCAGAGAGGAGAGCTTGACAGAGAGCCCTTACATC	840
QY	987	CAGGACTCGAGAGAGAGAGCTGCGGAGAGCGCTGCGGAGCCACAGAGAGCGCCAAACC	1046
Db	841	CAGGACTCGAGAGAGAGAGCTGCGGAGAGCGCTGCGGAGCCACAGAGAGCGCCAAACC	900
QY	1047	ATCTTCTCCCTGCGCAAGAGACCTCCGCGAGAGGCGAGGCGCTCCGGTGCATGAG	1106
Db	901	ATCTTCTCCCTGCGCAAGAGACCTCCGCGAGAGGCGAGGCGCTCCGGTGCATGAG	960
QY	1107	GAGAGAGAGATGTTGAGCTGCACTGCTGCGACTACGTAAAGACTTCCAAATGTACAAG	1166
Db	961	GAGAGAGAGATGTTGAGCTGCACTGCTGCGACTACGTAAAGACTTCCAAATGTACAAG	1020
QY	1167	GACCGCATCGAGGCCATCTCTGTGAGATGAGAGAGTTCGCATTGACCGGAGCACAAGC	1226
Db	1021	GACCGCATCGAGGCCATCTCTGTGAGATGAGAGAGTTCGCATTGACCGGAGCACAAGC	1080
QY	1227	ACACAAATGAGAGGGGCTGTGA 1247	
Db	1081	ACACAAATGAGAGGGGCTGTGA 1101	
RESULT 7			
US-09-798-412-1			
; Sequence 1, Application US/09798412			
; Publication No. US20030109428A1			
; GENERAL INFORMATION:			
; APPLICANT: Bertin, John			
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
; TITLE OF INVENTION: PROTEIN FAMILY AND USBS THEREOF			
; FILE REFERENCE: 07334-327001			
; CURRENT APPLICATION NUMBER: US/09/798,412			
; CURRENT FILING DATE: 2001-03-02			

```

; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)...(1720)
US-09-798-412-1

Query Match      48.7%; Score 1060.2; DB 11; Length 1879;
Best Local Similarity 76.2%; Pred. No. 1.6e-247;
Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4

Db      76 GCGGCCCAAGGCTCCTGGTGTGTCTGACATGACAGGTGAGTGGTCTCTGGAAGACCTCAGCCTGC 135
        46 GTGCCCATATGCCACAGGACGATCCAGCTGGCAGGAGTGGCTCCACAGACCTGAG---GC 101

Qy      136 CTGCTGAGGCCATGTGGACTACGAAACGATGACGAGTGTCTGGAAGCTCTCGAGGGCT 195
Db      102 CTACAGAGACATGTCAACTATGAAATATGACGAGAGTGTGGAGTGCCTCGGAGAGGT 161

Qy      196 TCCGGGTACGCTCACTTCGGGTATCGACCCCTACGCGATACACCTTAACCTGCGGCGAGT 255
Db      162 TCCGGGTAACTATCTCTGTCAATGACCCCTCAGCAATCACACCTTATCGCGCAGT 221

Qy      256 GCAAGGTCTTGAAACCTTGATGATGAGAGCAGTGTCTCAGCGACCCCAACCTGTCTATCC 315
Db      222 GCAAGTCTTGAAACCCCGATGATGAGAGCAGTGTCTCAGTGAACCCCAACCTGTCTATCC 281

Qy      316 GCAAGCGAAAGTGGGTGTGTCTCTGACATCTTGACGCGACCCGACCAAGGGCTACG 375
Db      282 GCAAGCGAAAGTGGGTGTGTCTCTGACATCTTGACGCGACCCGACCAAGGGCTACG 341

Qy      376 TGGCCTTCTTGAGAGCCTGGAAGCTTACTACCCGACGCTGTACAAGAAAGTCAAGGCA 435
Db      342 TGGCCTTCTTGAGAGCTCTGGAACCTCTACTACCCCTCAAGTTATACAGAAAGTCAAGGCA 401

Qy      436 AGGAGCCGCGCCGCTCTTCTTCATGATCATGAGCGCTCGGGGAGTCAAGGCTTGACTC 495
Db      402 AGGAGCCGCGGCTGTCTTCTTCATGATCATGAGCGCATCAAGGGGAGTGTGGGCTTGACGC 461

Qy      496 AGCTCTATGATGATAGGTCATGAAGTCGACGAAGAGTGACAGGACCTGACCGCGCTCG 555
Db      462 AGCTCTATGATGACAGGTCATGAAGTCGACGAAGAGGTTACGAGCTTGACGCGCTTTC 521

Qy      556 TGAGTCTCAAGATGATCTTTCATCAAGAGAGCTCGGGTGAAGACAGCCTGTCGCAAC 615
Db      522 TGAGTCTCAAGATGATCTTTCATCAAGAGAGCTGAAGGTTAAGGACAGCCTCTGCGCAAC 581

Qy      616 ACCAGAGCGTGTGACAGAGGCTCAAGAGAGAGTGCAGAGCCGACGCGAGCTCAAGC 675
Db      582 ACCAGAGCGGTTGACAGCGGCTCAAGAGAGAGTGTGAGCTGACAGTCCGAGCTGAAC 641

Qy      676 GCTGCAAGAGAGAACTTACGACCTGGCCATGCGCTTGGCGACCAAGAGTGAAGAGAAAG 735
Db      642 GCTGCAAGAGATAGAACTTACGACCTGGCCATGCGCTTGGCTCACTGAAGTGAAGAAAG 701

Qy      736 GCGCGCGCGTCAATGGGAAACGTTGACCTGACAGCTGAGATTGACCAAGCTCAAGCAAGCC 795
Db      702 GAGCGCACTATATGGGAAACGTTGACCTGACAGCTGAGATTGAGCTGACCAAGCTCAAGCAAGCC 761

```

```

QY 796 TCATGAGGCGGAGGACGACTGAGTGGAGCGGACGACGCTGAGCTCAGGACG 855
DB 762 TATGAGGACGAGGATGACTGAGGAGTGAAGCGAACAACACTGAAAGCTCCGACG 821
QY 856 CCATGAGAGGAGCGGCGCCAGACGAGAGCTGTGGAGCTGACAGAGGAGAGGCGCTGCG 915
DB 822 CCATGAGAGGAGCGGCGCTACGAGAGCTGTGGGACCTGACAGAGAGAGGAGCTTGT 881
QY 916 TCCAGGCGCGGAGTGCAGAGCTGAGAGCGCTCCGTCCAGAGGAGGAGGAGCTGACAGAGCA 975
DB 882 TCAGAGCGCGGAGTGCAGAGCTGAGAGCTCCGTCCAGAGGAGGAGGAGCTGACAGAGCA 941
QY 976 GCGCCCTACATCCAGGATCTGAGAGAGGATGGCGGAGCGGCTGCGGAGCCACAGAGAGC 1035
DB 942 GCGCCATACATCCAGGATCTGAGAGAGGAGGAGCTGCGGAGCTGACAGAGCAACAGAGAGC 1001
QY 1036 AGGCGCAACGCAATCTTCTCCGCGCAGAGACCTCCGCGAGGAGGAGGCGGAGCGCTCC 1095
DB 1002 AGGCGCAACGCAATCTTCTCCGCGCAGAGACCTCCGCGAGGCTGAGAGCGCTCCGAGACC 1061
QY 1096 GGTGATGAGAGGAGAGAGATGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1155
DB 1062 GGTGATGAGAGGAGAGAGATGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1121
QY 1156 AGATGTACAAAGGACCGCATGAGAGCCATCTGCTGAGATGAGAGAGAGTGCATTTAGC 1215
DB 1122 AGATGTACAAAGGACCGCATGAGAGCCATCTGCTGAGATGAGAGAGAGTGCATTTAGC 1181
QY 1216 GGGACCAAGACACAAATGAGAGGAGCTGTGACAGAGCTCCGCGCGAGGAGCTTGTAGCT 1275
DB 1182 GGGAC----- 1186
QY 1276 CCGCGAGAGCTGTGTGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1335
DB 1187 ----- 1186
QY 1336 CCCTCATGAGGAGTCCGCTGTGTGTGCTGTCCGCTCAGAGGCGCATAGCGAGGAGAGCTG 1395
DB 1187 -----CAGGCTATGACCTCAAGAGGAAAGCTG 1213
QY 1396 CACGCAACGACGCGCGGCGCTGACGAGAGAGAGAGAGCGCTGCGCAAGAGAGTGGCGAG 1455
DB 1214 CATGCAACAGTGTGCGCAAGGCTTTCAGACAAAGATTAAGCTCGAAAGAGAGGTTGAGAA 1273
QY 1456 CTGGGAGAGAGGCGGATGAGCTGAGCTGAGAGTGTTCAGTGTGAGAGCGAGCTACTG 1515
DB 1274 CTGGATGAGAGGCGGACAGATGAGCTGAGAGCTGTTCAGACGAGAGCGGAGTACTG 1333
QY 1516 GCGGTGAGAGGAGGCTCAGCGGCGGAGAGCTGAGAGAGCTGCTGCTGAGCTCCGAGCTG 1575
DB 1334 GCGGTGAGAGGAGGACTCAGAGAGAGAGAGCAATGAGAGTGTCACTGTGAGCTTGAAGCTT 1393
QY 1576 GAGATGAGCTCAGCGGAGAGTCCAGAGAGCTCTCAGCTCCCGAGAGCT--GAGAGAGC 1632
DB 1394 GAGAGAGATGCTCCCGAGAGAGCTCCAGAGAGCTTCACTGCTCAGAGAGCTGAGAGAGAT 1453
QY 1633 ACCAGAGCTTCAAGACAAAGGCTGCTTGCAGGCGGAGGAGGCGGAGAGAGGCTTTTGA 1692
DB 1454 GCGCAGAGCTCAGACAAAGGCTGCTGAGAGAGAGGAGAGGCGGAGAGGCTTTCGAG 1513
QY 1693 GCTGTGACCAAGAGAGGTTTTCGAGAGAGGCGGAGAGGCGGAGAGGCGGAGAG 1752
DB 1514 GTTCTGAAACAAGAGATCTTTCAGAGAG--CCCAAGACAGAGTGTCCAGAGAGAGCGAG 1570
QY 1753 CCGCGCGAGAGAGAGGCGGCGGCGCTCAAGAGAGTTCAGAGAGTTCAGAGAGAGGCGC 1812
DB 1571 CCGCGCGAGAGAGAGGCGGCGGCGCTCAAGAGAGGCTTTCAGAGAGTTCAGAGAGAGGCG 1630
QY 1813 GCGCTCAGAGAGAGTGCAGAAAGGATGCGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1872
DB 1631 GCGGCTCCGAGAGATGAGAGAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
QY 1873 GCGAGCGACACACGACAGCTGAGAGGCTCTTACGCGGAGAGAGAGTTCCTCCGAGAGCTGCGC 1932

```

```

DB 1691 GCGAGCGACACACCGACAGAGGAGGCTCTTACAGAGACAGCGGAGAGTGTGTGT 1750
QY 1933 TGACTTGCGCTTGAAGC 1949
DB 1751 GTAATGTGAAGGATG 1767

RESULT 8
US-10-325-917-1
; Sequence 1, Application US/10325917
; Publication No. US20030113787A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 0734-327001
; CURRENT APPLICATION NUMBER: US 10/325,917
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 09/798,412
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)...(1720)
US-10-325-917-1

Query Match 48.7%; Score 1060.2; DB 15; Length 1879;
Best Local Similarity 76.2%; Pred. No. 1.6e-247;
Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4;

QY 76 GCGGCGGAGGCTCTGAGTGTGTCTGAGAGTGTGCTCTGAGAGAGCTCTGAGAGCTGCG 135
DB 46 GTGCGCATAGCCAGGAGAGATCCAGCTGGAGGTGCTCCACAGAGACCTGA-----GC 101
QY 136 CTGCTGAGGCGATGTGAGACTACGAGAGACGATGACGAGTGTGAGAGCTGCTGAGAGCT 195
DB 102 CTACAGAGAGATGTACAGACTATGAAATGACGAGAGTGTGAGAGGCTGAGAGAGCT 161
QY 196 TCCGGGTACGCTCACTGCTGTATGACAGCTTACAGAGATGACCTTACTGCGGAGT 255
DB 162 TCCGGGTACGCTCACTGCTGTATGACAGCTTACAGAGATGACCTTACTGCGGAGT 221
QY 256 GCAAGTCTGAAACCTGATGATGAGAGAGAGTGTCAAGGACCCCAACCTGATCTCC 315
DB 222 GCAAGTCTGAAACCTGATGATGAGAGAGAGTGTCAAGGACCCCAACCTGATCTCC 281
QY 316 GCAAGGAGAGAGTGTGTCTCTGAGACATCTGACGAGAGAGGCGACAGAGGCTTACG 375
DB 282 GCAAGGAGAGAGTGTGTGTCTCTGAGACATCTGACGAGAGAGGCGACAGAGGCTTACG 341
QY 376 TGGCTTCTTGAAGAGCTGAGAGCTTACCTACCCGAGCTGTACAGAGAGTCAAGGCA 435
DB 342 TGGCTTCTTGAAGAGCTGAGAGCTTACCTACCTCAGTTATACAGAGAGTCACTGCA 401
QY 436 AGGAGCGGCGCGGCTTCTTCCATGATGATGAGAGGCTCCGAGGAGTCAAGGCTGATC 495
DB 402 AGGAGCGGCGCGGCTTCTTCCATGATGATGAGAGGCTCCGAGGAGTCAAGGCTGATC 461

```

QY 496 AGCTGCTATGATCTGAGGTCTATGAACTGCAGAGAGAGTGCAGACCTTGA CCGCTGC 555
 Db 492 AGCTCTATATGACAGAGGTCTATGAACTGCAGAGAGAGTTCAGAGCTTGA CCGCTGC 521
 QY 556 TGAGTCTCAAGATATCTTTCATCAAGAGCTGCGGGTGAAGACAGCTTGTGGCAAGC 615
 Db 522 TGAGTCTCAAGATATCTTTCATCAAGAGCTGAGGGTAAAGACAGCTTGTGGCAAGC 581
 QY 616 ACCAGAGAGGTGTGAGAGAGGTCAAGAGAGAGTGAAGCCGGCCGAGCTCAAGC 675
 Db 562 ACCAGAGAGGTGTGAGAGAGGTCAAGAGAGAGTGTAGCTTGAAGCTCAAGCTCAAGC 641
 QY 676 GCTGCAAGAGAGAGATACAGACTGCGCATGCGCTGCGCAGCAAGAGTGAAGAGAG 735
 Db 642 GCTGCAAGAGATAGAACTTACAGCTGCGCATGCGCTGCGCTCAAGTGAAGAGAG 701
 QY 736 GCGCCGCTCATGCGGAAACCGTGA CTTGACAGTGAAGATTGACCAAGCTCAAGCAAGC 795
 Db 702 GAGCAGCACTCATGCGGAAACCGTGA CTTGACAGTGAAGATTGACCAAGCTCAAGCAAGC 761
 QY 796 TATGAAAGCCGAGAGACAGACTGCAAGGTGAGAGCCGAGCAACGCTGAAGCTCAGAGC 855
 Db 762 TATGAAAGCCGAGAGATGATGCAAGGTGAGAGCCGAGCAACGCTGAAGCTCAGAGC 821
 QY 856 CCATGAGAGAGCGGCCAGCCAGAGCTGTGTGAGAGCTGAGAGAGAGAGCCCTGC 915
 Db 822 CCATGAGAGAGCGGCCAGCCAGAGCTGTGTGAGAGCTGAGAGAGAGAGAGCTGTGT 881
 QY 916 TCAGAGCCCGGGTGCAGAGAGCTGAGAGCTCCGTCAGAGAGAGAGAGTGCAGAGAGCA 975
 Db 882 TCAGAGCCCGGGTGCAGAGAGCTGAGAGCTCCGTCAGAGAGAGAGAGTGAAGTCAAGAGAT 941
 QY 976 GCCCTTACATCCAGGTACTGAGAGAGAGCTGAGAGAGCTGCGGAGCGCTGCGGAGCAACAGAGAGC 1035
 Db 942 GCCCTTACATCCAGGTACTGAGAGAGAGCTGAGAGAGCTGCGGAGCGCTGCGGAGCAACAGAGAGC 1001
 QY 1036 AGGCCAACCCTTTCTTCCCTGCGCAAGAGACTCCGCAAGAGAGAGAGCCGAGCGCTCC 1095
 Db 1002 AGGCCAACCCTTTCTTCCCTGCGCAAGAGACTCCGCAAGAGAGAGAGAGAGAGAGAGCC 1061
 QY 1096 GGTGATGAGAGAGAGAGAGATGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGAGAGCTGCA 1155
 Db 1062 GGTGATGAGAGAGAGAGAGATGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGAGAGAGCTGCA 1121
 QY 1156 AGATGTACAGAGAGAGAGAGCTGAGAGAGAGCTGAGCTGAGCTGAGAGAGAGAGTGCCTTGAAGC 1215
 Db 1122 AGATGTACAGAGAGAGAGAGCTGAGAGAGAGCTGAGCTGAGCTGAGAGAGAGAGTGCCTTGAAGC 1181
 QY 1216 GGGACCAAGACACAAATGAGAGGGGCTGTGACAGAGCTCCGCGCCAGCGGCTTGAAGCT 1275
 Db 1182 GGGAC----- 1186
 QY 1276 CTTCCGAGAGCTTGTGCTTGAAGTTGGGGGGCCGAGGCCAGAGGCAAGCTTGGAG 1335
 Db 1187 ----- 1186
 QY 1336 CCTCACTGAGAGGTGAGCTTGTGCTTCCGTCAGAGCAAGTCAAGCCAGAGAGAGAGCTG 1395
 Db 1187 -----CAGGCTATGACTTCAAGAGAGAGAGCTG 1213
 QY 1396 CACGACACAGCAGCCCGGGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1455
 Db 1214 CACGACAGAGTGTGCGCAAGCTTTCAGAGCAAGAGATGAGCTGCAAGAGAGAGAGTTCAGAG 1273
 QY 1456 CTGGGAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGAGAGAGAGAGAG 1515
 Db 1274 CTGGATGAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGAGAGAGAGAGAGAGAG 1333
 QY 1516 GCGGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1575
 Db 1334 GCGGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1393

QY 1576 GAAGATGCTCACCCAGAGAGTCCAGAGAGCTTCACTCCCCAGAGAGCT---GAGAGAC 1632
 Db 1394 GAAGACAGATTCCTCCAGAGAGAGTCCAGAGAGCTTTCAGCTGCTCAGAGAGAGAGAGAT 1453
 QY 1633 ACCAGGCTCACAAGAGAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1692
 Db 1454 GCGGAGTCTCAAGAGAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1513
 QY 1693 GCTGTGACAGAGAGAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1752
 Db 1514 GTTCTGACAGAGAGAGAGTCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
 QY 1753 CCGCCGAG 1812
 Db 1571 CCGCCGAG 1630
 QY 1813 GCGCTCAG 1872
 Db 1631 GCGCTCAG 1690
 QY 1873 GCGAG 1932
 Db 1691 GCGAG 1750
 QY 1933 TGAAGTGTGAGAGAGAG 1949
 Db 1751 GTATTGTGAGAGAGAG 1767

RESULT 9

US-09-798-412-3

Sequence 3, Application US/09798412

Publication No. US20030109428A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-327001

CURRENT APPLICATION NUMBER: US/09/798,412

PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2000-12-01

PRIOR FILING DATE: 2000-10-10

PRIOR APPLICATION NUMBER: US 09/513,904

PRIOR FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: US 09/507,533

PRIOR FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: US 60/168,780

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1608

TYPE: DNA

ORGANISM: Rattus norvegicus

US-09-798-412-3

Query Match 48.0%; Score 1045; DB 11; Length 1608;

Best Local Similarity 77.9%; Pred. No. 7.6e-244; Indels 154; Gaps 3;

Matches 1370; Conservative 0; Mismatches 235;

QY 147 ATGTCAGACTACAG 206
 Db 1 ATGTCAGACTACAG 60

QY 207 CTGACCTGGTCTATGACAG 266
 Db 61 CTATCTCTGTCTATGACAG 120

QY 267 AACCTTATATATGAG 326
 Db 121 AACCTTATATATGAG 180

QY	327	GTGGGTGTCCTCCGGA	CATCTCGTAGGGAC	CCGGCCACAAGAGGCTACGTGGCCCTTCTC	386	
Db	181	GTGGGTGTCCTCCGGA	CATCTCGTAGGGAC	CCGGCCACAAGAGGCTACGTGGCCCTTCTT	240	
QY	387	GAGAGCCTGAGCTTACT	ACCAGGCTGTA	CAAGAAAGTCA	CAGGCMAAGAGCCGACC	446
Db	241	GAGAGTGGAACTCTACT	ACCCTCAGTTATA	CAGAAAGTCACTGGCAAGAGCAAGC	300	
QY	447	CGCGTCTTCTCCATGAT	CAATGAGCGCTTC	CGGGAGTCAAGGCTTGA	CTCACTCAGCTGTATG	506
Db	301	CGTGTCTTCTCCATGAT	CAATGAGCGCTTC	CGGGAGTCAAGGCTTGA	CTCACTCAGCTGTATG	360
QY	507	ACTGAGGTTCATGAAG	CTGCAGAAAGGTG	CAGAGACCTGACCGGCTGTAGCTCCAA	566	
Db	361	ACAGAGTTCATGAAG	CTGCAGAAAGGTTC	AGAGCTGACCGGCTGTAGCTCCAA	420	
QY	567	GATGACTTCATCAAG	AGAGCTCGGGTGA	AGGACAGCTCTGCGCAACACAGAGAGCT	626	
Db	421	GATGACTTCATCAAG	AGAGCTAGAGGTAA	AGGACAGCTCTGCGCAACACAGAGAGCT	480	
QY	627	GTGCAGAGCTTCAG	AGAGAGTGCAGAGCC	CGGACGCGAGCTTCAGAGCTTCAGAGAG	686	
Db	481	GTGCAGAGCTTCAG	AGAGAGTGTAGCT	GAGAGTGCAGAGCTTCAGAGAGT	540	
QY	687	GAGAACTTCAGAC	CTGGGCCATCGCT	CGCTGCTCACTGAGTGAAGAAAGGAGCAGACTTC	746	
Db	541	GAGAACTTCAGAC	CTGGGCCATCGCT	CGCTGCTCACTGAGTGAAGAAAGGAGCAGACTTC	600	
QY	747	ATGCGGAACCGGAC	CTGAGCTGGAGTTA	CAACAGCTCAAGGCACAGCTCATGAGGCC	806	
Db	601	ATGCGGAACCGGAC	CTGAGCTGGAGTTA	CAACAGCTCAAGGCACAGCTCATGAGGCC	660	
QY	807	GAGAGCACTGCAAG	TGAGTGGAGCGGAC	ACACGCTGAACTCAGGACAGCCATGAGAGAG	866	
Db	661	GAGAGTACTGCAAG	TGAGTGGAGCGGAC	ACACGCTGAACTCAGGACAGCCATGAGAGAG	720	
QY	867	CGGCCAGCCAGAG	AGCTGCTGTGGAGCT	GACAGAGAAAGCCCTGCTCCAGGCCCGG	926	
Db	721	CGGCCAGCCAGAG	AGCTGCTGTGGAGCT	GACAGAGAAAGCCCTGCTCCAGGCCCGG	780	
QY	927	GTGCAGAGCTGAGAG	CTCCGCTCA	AGAGGGGAAAGCTGAGACAGAGAGAGCCCTTACATC	986	
Db	781	GTGCAGAGCTGAGAG	CTCCGCTGAGAGGGGTAA	CTACACAGAAATAGCCATACATC	840	
QY	987	CAGGTACTGAGAGAG	ACTGGCGGACGCTGCGGGAC	CCACAGAGACAGAGCCAAACCC	1046	
Db	841	CAGGTGCTGAGAGAG	ACTGGCGTTCAGGCA	CTGACAGAAACACAGAGACAGAGCCACGACCC	900	
QY	1047	ATCTTCTCTCCGCA	AGAGACTTCGCGAGGAG	CGAAGCCCGACGCTCCGTTGATGAGAG	1106	
Db	901	ATCTTCTCTCCGCA	AGAGACTTCGCGAGGAG	CGTCCGAGCTTCGAGCCCGGTTGATGAG	960	
QY	1107	GAGAAAGAGATGTT	CGAGCTGCAATGCTGGCA	CTACGTAAGAGATCCAAATGTACAG	1166	
Db	961	GAAAAGAGATGTT	CGAGCTGCAATGCTGGCTTGC	CCCAAGATGACCAAGATGATCAAG	1020	
QY	1167	GACCGCATCGAGG	CCATCTGCTGACATG	AGAGAGTGCAGCATTTGACCGGGACAGAGC	1226	
Db	1021	GACCGGATCGAGG	CCATCTGCTGACATG	AGAGAGTGTCTCATTTGACCGGGAC	1074	
QY	1227	ACACAAATGAGG	GGGTGTGAC	CAGACTCCGCGCCACAGCGCTTGA	CGCTCTCCGGAAGCC	1286
Db	1075	-----	-----	-----	-----	1074
QY	1287	TCTGCTTGAATTTG	GGCGGACCGGCGAGG	CCCAAGGCAAGCTTTGGGCGCTCATGAG	1346	
Db	1075	-----	-----	-----	-----	1074
QY	1347	GGTGGGCTTTGCTG	TCCCGGTCAAGGCC	ATAGCCACGGGGAGAGAGCTGCACGACACGA	1406	
Db	1075	-----	-----	-----	-----	1112

QY	1407	CGCCCCGGGGCTTGACAGGAAGAAGACGGCTGCGCCCAACACAGTGGGGAGCTGGGCCAGAA	1466
Db	1113	TGCCCCAAGCTTTTAGACCAAAAGTAAGCTGCGCAAGACAGGTTGAGAACTGATGAGAA	1172
QY	1467	GCGCGATGAGCTGACAGCTGCAGGTGTTCCAGTGTGAGCGCCAGCTACTGCGCGTGAAGG	1526
Db	1173	GGCGGACGAGTTGACGTTGACGCTGTTCCAGACCGAAGAGCGATTACTGGCGCGTGAAGG	1232
QY	1527	CAGGCTCAGGGCGGACAGACGACTGAGACGCTGCTGTGAGCTCCGACTGGAAGATGCTC	1586
Db	1233	CAGACTCAAGGACGACGAATTTGACATGCTCATCTCTAGCTCTGACTTTGGAAGACATTC	1292
QY	1587	ACCCAGAGAGTCCCGAGAGCTCTCACTCCCGCCAGAACCT--GAGAGACACCCAGCTCTC	1643
Db	1293	CCCTGAGAACTCCACGAGGCTTTTCACTGCTCCAGAACCTGAGAGAGGATGCCAGCTCTC	1352
QY	1644	AGACAAAGGCGCTGCGCTTCCCGGCGGGGGAGCGCCGAACAGCCCTTTGCACTGTGCACA	1703
Db	1353	AGACAAAGGCTGCTCTTGCGACGACGAGGAGCCACAGACAGCCCTTCTGTGTTCTGAACAA	1412
QY	1704	GGAGCAGGTTTTTGCGGAACCCCACTGACGAGGCTTGACAGCGCGGAGCGCCGCCAGAA	1763
Db	1413	GAAACATCTTTTCGAGACA--CCATGACAGGTGTGCCAGACAGACGACGCCCCCGAGAA	1469
QY	1764	GGAGCGGCGCGGCTCTCAAGAGAGTTTGAACCTACCGCAGGAAGCGCGCCCTCAGAA	1823
Db	1470	GGAGCGGCGGCGCTCTCAAGGAGAGCTTCGAGAACTACCGCAGGAAGCGGCGCTCCGCAA	1529
QY	1824	GATCCAGAAAGATGTGCGGCGCAAGGGGAGGAGACCCGGGAGAACACACAGGCGACGCAAA	1883
Db	1530	GATCCAGAAAGATGTGCGGCGCAAGGAGAGAGGGATCACGGGAATTACAGACGGCAGCGCAA	1589
QY	1884	CACCGACACTGAGGCGCTCC	1902
Db	1590	CACCGACACCGAGGCGCTCC	1608

```

RESULT 10
US-10-325-917-3
; Sequence 3, Application US/10325917
; Publication No. US20030113787A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-327001
; CURRENT FILING DATE: US/10/325,917
; PRIOR APPLICATION NUMBER: 2002-12-20
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/798,442
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Rattus norvegicus
;
Query Match          48.0%; Score 1045; DB 15; Length 1608;
Best Local Similarity 77.9%; Pred. No. 7,6e-244;
Matches 1370; Conservative 0; Mismatches 235; Indels 154; Gaps 3

```

```

Db      1 ATGTCAAGCTATGAAAAATGACGACAGTGTGAGTGTCCCTGGAGAGCTTCGGGTTGAG 60
Qy      207 CTACGCTGCTGATCGACCCCTCAAGCATCAACCTTACCTGGGCGAGTGCAGAGTCTCTG 266
Db      61 CTAATCTGTGATGATGACCCCTCAAGATCAACCTTATCTGCGCCAGTGCAGAAAGTCTG 120
Qy      267 AACCTGATGATGAGAGAGAGAGTGTCTAGACGACCCCAACCTGTCTATCCGCAAGAAA 326
Db      121 AACCCGATGATGAGAGAGAGTGTCTAGTACCCCAACCTGTGTCTATCCGCAAGAAA 180
Qy      327 GTGGGTGTGCTCTGAGACATCTCTGACGAGACCGGCGCAAGAGGCTAAGTGGCTTCTC 386
Db      181 GTGGGTGTGCTCTGAGACATCTCTGACGAGGACAGGCCCAAGAGGCTAAGTGGCTTCTC 240
Qy      387 GAGAGCCTGAGAGCTCTACTACCCGAGCTGTACAAAGAGTCAAGGCAAGAGAGCCGCGC 446
Db      241 GAGAGCTGGAACCTTACTACCTCAGTTATACGAAAGTCACTGGCAAGAGAGCCAGCG 300
Qy      447 CGCGCTTCTCATGATCATGACGCGTCGGGGAGTCAAGGCTGTACTCACTGAGTGTATG 506
Db      301 CGTGCTTCTCATGATCATGACGATCAGGGAGTGTGGGCTGTAGCGAGCTGTATG 360
Qy      507 ACTGAGTCTATGAAGCTGACAGAAAGGTGACAGACCTGACCGGCTGTAGTCTCAAA 566
Db      361 ACAGAGTCTATGAAGCTGACAGAAAGTTCAGAGCTGTAGAGGCTTCTGAGTCTCAAG 420
Qy      567 GATGACTTCAATCAAGAGAGCTGCGGAGTGAAGAGACGCTGTGCGAAGACACAGAGAGT 626
Db      421 GATGACTTCAATCAAGAGAGCTGAGGGTAAAGACAGAGCTCTGCGAAGACACAGAGAGT 480
Qy      627 GTGCAAGAGCTCAAGAGAGAGTGTGAGGCGGACCGGAGCTCAAGCGCTGTAAAGAG 686
Db      481 GTGCAAGCGCTCAAGAGAGAGTGTGAGTGTGAGAGTGTGCGAGCTGTAAAGAGT 540
Qy      687 GAGAAGCTACAGCTGAGAGCTGAGCGCTGCGCGACAGAGTGTGAGAGAGGGCGCGGCTC 746
Db      541 GAGAAGCTACAGAGCTGAGAGCTGAGCGCTGCGCTGCTACCTGAGTGAAGAGAGAGAGAGCTC 600
Qy      747 ATGCGGAAGCTGTGACCTGTGACAGCTGAGAGTGTGACAGCTCAAGCAAGCTCATGAGAGC 806
Db      601 ATGCGGAAGCTGTGACCTGTGAGAGCTGTGAGAGCTCAAGAGCTCAAGCTCATGAGAGC 660
Qy      807 GAGAGCACTGTGCAAGTGTGAGAGCTGACAGCAAGCTGTAAAGTGTGAGAGAGCGCATGAGAG 866
Db      661 GAGAGTGTGCTCAAGTGTGAGAGCTGACCAACACACTGAAGCTCCGAGAGCGCATGAGAG 720
Qy      867 CGGCGCAAGCTGAGAGCTGTGAGAGTGTGACAGAGAGAGAGCGCTGTGCAAGCGCGG 926
Db      721 CGGCGCAAGCTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGAGAGAGAGAGAGAGCGCGG 780
Qy      927 GTGCAAGAGCTGAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 986
Db      781 GTGCAAGAGCTGAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 840
Qy      987 CAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1046
Db      841 CAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 900
Qy      1047 ATCTTCTCTCTGCGAAGAGAGCTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1106
Db      901 ATCTTCTCTCTGCGAAGAGAGAGCTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy      1107 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1166
Db      961 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy      1167 GAGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1226
Db      1021 GAGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1074
Qy      1227 ACACAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1286

```

```

Db      1075 ----- 1074
Qy      1287 TGTGCTGAGAGTGTGGGCGGCGCGGCGGAGAGGCGCAAGGGAAGCTTGTGGGCGCTCACTGAG 1346
Db      1075 ----- 1074
Qy      1347 GGTGGGCTTGTGCTGTCCCTGAGGCGCATAGACAGCGGAGAGAGAGAGAGAGAGAGAGAG 1406
Db      1075 ----- CAGGCTATGAGCTCAAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1112
Qy      1407 CGCGCGGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1466
Db      1113 TGCCCAAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1172
Qy      1467 GGGGATGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1526
Db      1173 GGGCGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
Qy      1527 CAGGCTCAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1586
Db      1233 CAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292
Qy      1587 ACCGAGAGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
Db      1293 CCGCAGAGAGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1352
Qy      1644 AGACAAAGAGCTGTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
Db      1353 AGACAAAGAGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1412
Qy      1704 GAGAGAGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
Db      1413 GAGAGAGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1469
Qy      1764 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1823
Db      1470 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1529
Qy      1824 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
Db      1530 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1589
Qy      1884 CACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1902
Db      1590 CACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1608

```

RESULT 11
 US-10-032-159A-5
 / Sequence 5, Application US/10032159A
 / Publication No. US20020164703A1
 / GENERAL INFORMATION:
 / APPLICANT: Pawlowski, Krzysztof
 / APPLICANT: Reed, John C.
 / TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
 / FILE REFERENCE: P-LJ 5100
 / CURRENT APPLICATION NUMBER: US/10/032,159A
 / PRIOR FILING DATE: 2001-12-19
 / PRIOR APPLICATION NUMBER: US 60/257,457
 / NUMBER OF SEQ ID NOS: 37
 / SOFTWARE: PastSeq for Windows Version 4.0
 / SEQ ID NO 5
 / LENGTH: 432
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1)...(432)
 US-10-032-159A-5

Query Match 19.9%; Score 432; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.9e-95;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 CTGGGCAAGCACCAGAGCGTGTGAGAGGCTCAAGAGAGAGTCCGAGCGCCGAGCGCC 665
DB 1 CTGGGCAAGCACCAGAGCGTGTGAGAGGCTCAAGAGAGAGTCCGAGCGCCGAGCGCC 60
QY 666 GAGCTCAAGCGCTGCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 725
DB 61 GAGCTCAAGCGCTGCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 120
QY 726 GAGGAGAGAGGCGCGCGCTCAAGAGAGAGTCCGAGCGCCGAGCGCC 785
DB 121 GAGGAGAGAGGCGCGCGCTCAAGAGAGAGTCCGAGCGCCGAGCGCC 180
QY 786 AAGCAGAGCGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 845
DB 181 AAGCAGAGCGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 240
QY 846 CTGAGAGAGCGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 905
DB 241 CTGAGAGAGCGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 300
QY 906 AAGCGCTGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 965
DB 301 AAGCGCTGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 360
QY 966 GACAGAGAGAGCGCTCAAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 1025
DB 361 GACAGAGAGAGCGCTCAAGAGAGAGTCAAGAGAGTCCGAGCGCCGAGCGCC 420
QY 1026 CACCAAGAGAGAG 1037
DB 421 CACCAAGAGAGAG 432

RESULT 12
US-10-032-159A-7
; Sequence 7, Application US/10032159A
; Publication No. US20020164703A1
; GENERAL INFORMATION:
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
; TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: P-12 5100
; CURRENT APPLICATION NUMBER: US/10/032,159A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/257,457
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3744
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3744)
US-10-032-159A-7

Query Match 17.3%; Score 375.8; DB 14; Length 3744;
Best Local Similarity 56.9%; Pred. No. 2.4e-81;
Matches 817; Conservative 0; Mismatches 547; Indels 73; Gaps 4;

QY 157 ACGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
DB 26 AGGATGAG 85
QY 217 TCATGAG 276

DB 86 ATATCAACCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 145
QY 277 ATGAG 336
DB 146 ATGAG 205
QY 337 TCCTGAG 396
DB 206 TGTTGAG 265
QY 397 AGCTTACATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 456
DB 266 AATTATTAATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 325
QY 457 CCATGATCATGAG 516
DB 326 CCATGATCATGAG 385
QY 517 TGAAGCTGCAAG 555
DB 386 TGAAGCTGCAAG 445
QY 556 TGAAGCTGCAAG 615
DB 446 TGAAGCTGCAAG 505
QY 616 ACCAG 675
DB 506 ACCAG 565
QY 676 GCTGAG 735
DB 566 GCTGAG 625
QY 736 GCGCGCGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795
DB 626 GCGCGCGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 685
QY 796 TCATGAG 855
DB 686 TCATGAG 745
QY 856 CCATGAG 915
DB 746 CCATGAG 805
QY 916 TCATGAG 966
DB 806 TCATGAG 865
QY 967 ACAAG 1026
DB 866 ACAAG 925
QY 1027 ACAAG 1086
DB 926 ACAAG 985
QY 1087 GAGCGCTCCGAG 1146
DB 986 GAGCGCTCCGAG 1045
QY 1147 AGAGCTCAAG 1206
DB 1046 AGAGCTCAAG 1105
QY 1207 CAATTGAG 1266
DB 1106 CAATTGAG 1127
QY 1267 GCTTGAAG 1326
DB 1128 GCTTGAAG 1182

QY 1227 AGCTTGAGGGCCCTCACTCAGGAGGATCGAGCTTGAGCTGCCGTCAGGCCATAGCACGGCG 1386

Db 1183 AGCAAGGGTCCGACCATCGCTCTGTATCGCGTTATATGAAGAGGCCCTTCACCTCCGCA 1242

QY 1387 GAGGAGCTGCACGCACACAGCAGCCCGGGGCTCGCAGAGAAAGACCGCGCTGCAGACAG 1446

Db 1243 GATGAGCTCAGACACAGTACTCGCAGTGGCTTTATCGAAAAGGACAACTACAGGAGCAG 1302

QY 1447 GTGCGGAGCTGGGCGAGAAAGCGGATAGCTGCAGCTGCAGGTTTCCAATGTGAGCGC 1506

Db 1303 ATCCGCGAGCTGAGAGAAACAACGACGATGAGGATCGAGATGCTCGCGGGGAGGCGC 1362

QY 1507 CAGCTACGCGCGCTGAGAGGAGGACAGCTCAGGGGCGACAGCGTGGAGAGCGCTGTCTCG 1563

Db 1363 TGCATCGTCAACTGAGAGGACAGTGTGGGGCGCTTCTCCAGAGACAGCAACACTTG 1419

RESULT 13

```

US-09-798-412-12
? Sequence 112: Application US/09798412
? Publication No: US20030109428A1
? GENERAL INFORMATION:
? APPLICANT: Bellin, John
? TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
? TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
? FILE REFERENCE: 07334-327001
? CURRENT APPLICATION NUMBER: US/09/798,412
? CURRENT FILING DATE: 2001-03-02
? PRIOR APPLICATION NUMBER: US 09/728,260
? PRIOR FILING DATE: 2000-12-01
? PRIOR APPLICATION NUMBER: US 09/685,791
? PRIOR FILING DATE: 2000-10-10
? PRIOR APPLICATION NUMBER: US 09/513,904
? PRIOR FILING DATE: 2000-02-25
? PRIOR APPLICATION NUMBER: US 09/507,533
? PRIOR FILING DATE: 2000-02-18
? PRIOR APPLICATION NUMBER: US 60/168,780
? PRIOR FILING DATE: 1999-12-03
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 12
? LENGTH: 3441
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-798-412-12

```

Query March	17.1%;	Score 372.2;	DB 11;	Length 3441;
Best Local Similarity	60.5%;	Pred. No. 1.8e-80;		
Best Match 664; Conservative	0;	Mismatches 403;	Indels 30;	Gaps 2;

QY	157	ACGAGAAAGATGACAGAGGCTGTGAAAGCTTCGAGAGAGGCTCCGGGTGACGCTACCTCGG	216
Db	26	AGGATGAAGAGGACCCCTTTGTGTGGAAATGTGGATGTAAACCGGACATGCTCAGCCGCT	85
QY	217	TCATTCAGCCCTCCACGCATCAACCTTACTCTGGCAGTGCAGAGGTCTCGAACCTGTATG	276
Db	86	ATATCAACCTCGCAAGCTCAAGCCCTTACTGCTGCTAGTGTAGGTCAATTGATGACAGG	145
QY	277	ATGAGAGCAGGTGTTACGCAACCCCAACCTGTATCCGCACAAACGAAAGTGGGTGTC	336
Db	146	ATGAAGATGAAGTGGTTTATGCGCCCTTAATGCTGCATCCAAATCAACCGAAGAGGCCGCGC	205
QY	337	TCCGAGATATCCTGACAGCGGACCGGCAACAAGGCTAGCTGGCCTTCCTCGAGAGCCTGG	396
Db	206	TGTTGGACATTCTTATATCAATCCAGGGGCAAAAGGGCTATGTGTCTTTCTTGGAGACCTTAG	265
QY	397	AGCTTACTACCCGACGCTGTACAAAGAAAGTACACAGGACAGGAGCCCGGCTCTTCT	456
Db	266	AATTTTATTTACCCAGACCTGTACAAACGTGTACTCTGGGAAAGGCCCACTGGGAATTTCT	325
QY	457	CCATGATCATGACGCGCTCCGGGGAGTCAAGCCTTAATCACTGCTGTATGACTAGGTCA	516

Db	326	CAACCATTTGGTGTGGAGAAAGGCCACGAGGGCCCTCAAGCACTTCTGATGAAACGAGGTCA	385
OY	517	TGAAGCTGCAGAGAGAGGTGCAGAC-----CTGACCCGCTGC	555
Db	386	TCAAGCTGCAGACGACATGAAAGGCCAAGGACCTGCACCGCTGCGAGCTGCTGCCAGGT	445
OY	556	TGAGCTCCAAAGATGACTTCAATCAAGAGCTGCGGGTGAAGAGCAAGCCTGCTGCCAAGC	615
Db	446	TGCGGCAGCTGGAGAAATGAGAAAGAGAGATGACGTGACCGCGGTGGAAGTGTAACTT	505
OY	616	ACGAGAGCGGTGTCAGAGGCTCAAGAGAGAGTGCAGGCGCGGACGCGCAGGCTCAAGC	675
Db	506	TTCGAGAGCGGTACTTCAAGATGAAGAGAGGCGGACAGCTCAATATGACAGCTGGTCA	565
OY	676	GCTTCAAGAGAGAACTTACGACCTGGCCATGCGCTGCGCACACAGAGTGAGAGAGAG	735
Db	566	AGGTGAAGAGAGCAACATCAACTTTAGCCATGCGCTGACACAGCTCAGTGAAGAGAA	625
OY	736	GCGCGCGCTCATGCGGAAACCGTAGCTGCAGCTGAGATTGACAGCTCAAGCAAGCC	795
Db	626	ACATGCGCGGTATAGAGAGCGGAGACCTCCAACTCGAGATGATCAGTTAAGCACCGGT	685
OY	796	TCATGAAGAGCCGAGAGACGACTGCAGAGTGGAGCGCCAAAGCACACGCTGAAGCTCAGGCA	855
Db	686	TGAATTAGATGAGAGAGGATGTAAAGCTGGAGAGAAATCAGTCTTAAACTGAAGATG	745
OY	856	CCATGAGAGAGCGGCCCCAGCCAGAGAGCTGCTGTGGAGCTGCAACAGAGAGAGCCCTGC	915
Db	746	ACATTGAAAAATCGGCCCAAGAGAGAGAGGTTCTGGAACTGGAGCGGAGAGATGAAATGC	805
OY	916	TCCAGGCGCGGCTGACAGAGCTGAGAGCGTCCGTCCAGAGGGGAA-----GCTGG	966
Db	806	TGAAGACCAAAACACAGAGCTGAGTCCATTCATCCAGCGCGGAGAGCGACCTTGCCAG	865
OY	967	ACAGAGAGAGCGCCCTTCAATCCAGGTTACTGAGAGAGGACTGGCGGCAAGCGCTGCCGAC	1026
Db	866	ACTCAGACAAAGGCCATCCTGGAACATCTTGGAAACAGACCGCAAGAGAGGCCCTTGAAGACA	925
OY	1027	ACCAGAGAGAGGCCAACACCATCTTCTCCCTGCGCAAGAACCTTCGCCGCGGCGAGGCC	1086
Db	926	GGCAGAGAGCTGTCAACAGATCTAACACTGCAAGAGAGAGAGGCCCGCACGACAGGAGC	985
OY	1087	GACGCGCTCGGTGATGAGAGAGAAAGAGATGTTGAGCTGCAGTGCCTGGCACTACGTA	1146
Db	986	TGCAGACCAAGTACTCTGGAGAGAAAGAGAGGACTGGAGCTCAATGTCTCGACCTGGGAA	1045
OY	1147	AGGACTCCAAATGTACAAAGGACCGCATCGAGCCATCTCTCTCAATGGAAGAGGTGC	1206
Db	1046	AGGACTGTGAATGTACAAAGCACCGCATGAAACAGGTCTATGCTCACTGGAGAGGTGG	1105
OY	1207	CCATTGAGCGGAGCAAG 1223	
Db	1106	AGCGGAGCGGAGCACCG 1122	

RESULT 14

```

US-10-325-917-12
; Sequence 12, Application US/10325917
; Publication No. US20030113787A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-327001
; CURRENT APPLICATION NUMBER: US/10/325.917
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/09/798,412
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904

```

PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/507,533
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/168,780
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 3441
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-917-12

Query Match 17.1%; Score 372.2; DB 15; Length 3441;
Best Local Similarity 60.5%; Pred. No. 1.8e-80;
Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;

157 ACGAGAACGATGACGAGTCTGAAAGCTCTGAGAGGCTTCCGGGTGACGCTCACTCG 216
26 AGGATGAGAGAGAGCGCTTGTGGAGAGATGAGTGAACCGGCAATGCTCAGCGCT 85
217 TCATCGACCCCTCAGCATCAGCATCACTTACTGCGGAGTGCAGAGTCTGAAACCTGATG 276
86 ATATCAACCTCTCCAGAGCTCAGCCCTTACTGCTGCTAGTGTAAAGTCAATTGATGACAG 145
277 ATGAGAGAGAGTGTCTGAGCGAGCCCACTGCTGCTCAATCCGCAACGAAAGTGGTGTGC 336
146 ATGAGAGTGAAGTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 205
337 TCCTGACATCTCTGACAGCGAGCCGCAAGAGGCTACGTGCGCTTCTCTGAGAGCTG 396
206 TGTGGACATTTCAACATACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 265
397 AGCTTACTACCGGAGCTGTACAGAGGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 456
266 AATTTTATTCACGAGACTGTACAACTGGTGAATGGGAAAGCCCACTCGGAGATTCT 325
457 CCATGATCATGAGCGGCTCGGAGAGTCAAGGCTGATGCTGCTGATGATGATGATGATGATG 516
326 CCAACATTTGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 385
517 TGAAGCTGACAGAGAGTGCAGAGC-----CTGACCGCGCTGC 555
386 TCAAGCTGACAGAGAGATGAAGCCCAAGAGCTGCAAGCTGCGAGCTGCGCAGCT 445
556 TGAAGCTCAAGATGATCTTCAATCAAGAGCTGCGGCTGAAGAGCAGCTGCTGCGCAGC 615
446 TGGCGGAGCTGAGAGATGAGAGAGAGATGAGAGAGCTGAGAGCTGCTGAGCT 505
616 ACCAGAGAGCTGTGACAGAGCTCAAGAGAGAGTGCAGAGCGGAGCGGAGCTCAAGC 675
506 TCCAGGAGCGGTACTACAAATGAGAGAGAGAGGAGGAGCTCAATGAGAGAGCTGCTCA 565
676 GCTGACAGAGAGAGAGATGAAGAGCTGCGCTGCGCTGCGGAGCAGCAGAGTGAAGAGAG 735
566 AGGTGAAGAGAGAGAGATGAAGTGAAGAGAGATGAGTGAAGAGAGATGAGTGAAGAGAG 625
736 GCGCGCGCTCATGAGAGAGAGCTGAGAGCTGAGAGTGAAGTGAAGAGTGAAGAGAGAG 795
626 ACATGCGGCTCATGAGAGAGAGAGCTTCAACTGAGATGATCACTTAAGAGAGAGAGAG 685
796 TCATGAAGAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855
686 TGAATGAAGATGAGAGAGAGATGAAGTGAAGAGAGATGAGTGAAGAGAGATGAGTGAAG 745
856 CCATGAG 915
746 ACATTTGAAGATGAG 805
916 TCCAG 966
806 TGAAG 865

967 ACAG 1026
866 ACTCAG 925
1027 ACCAG 1086
926 GCGAG 985
1087 GAGCGCTCGGTGATGAG 1146
986 TCCGAG 1045
1147 AGAGCTCAAGATGATGAG 1206
1046 AGGAGCTGAAGATGATGAG 1105
1207 CCATGAG 1223
1106 AGCGGAG 1122

RESULT 15
US-09-798-412-10
Sequence 10, Application US/09798412
Publication No. US20030109428A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-327001
CURRENT APPLICATION NUMBER: US/09/798,412
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 09/728,260
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/685,791
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/513,904
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/507,533
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/168,780
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 4276
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (328) ... (3768)
US-09-798-412-10
Query Match 17.1%; Score 372.2; DB 11; Length 4276;
Best Local Similarity 60.5%; Pred. No. 1.8e-80;
Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;

157 ACGAGAACGATGACGAGTCTGAAAGCTCTGAGAGGCTTCCGGGTGACGCTCACTCG 216
355 AGGATGAG 412
217 TCATGAG 276
413 ATATCAACCTCTCCAGAGCTCAGCCCTTACTGCTGCTAGTGTAAAGTCAATTGATGAGCAG 472
277 ATGAG 336
473 ATGAG 532
337 TCCTGAGATCTCTGAG 396
533 TGTGGACATTTCAACATACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 592

